



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁷ : C12N	A2	(11) International Publication Number: WO 00/65025 (43) International Publication Date: 2 November 2000 (02.11.00)
<p>(21) International Application Number: PCT/US00/10828</p> <p>(22) International Filing Date: 21 April 2000 (21.04.00)</p> <p>(30) Priority Data: 60/130,691 23 April 1999 (23.04.99) US</p> <p>(71) Applicant (for all designated States except US): MERCK & CO., INC. [US/US]; 126 East Lincoln Avenue, Rahway, NJ 07065-0907 (US).</p> <p>(72) Inventors; and (75) Inventors/Applicants (for US only): AUSTIN, Christopher, P. [US/US]; 126 East Lincoln Avenue, Rahway, NJ 07065-0907 (US). BAILEY, Wendy, J. [US/US]; 126 East Lincoln Avenue, Rahway, NJ 07065-0907 (US). MA, Lei [CN/US]; 126 East Lincoln Avenue, Rahway, NJ 07065-0907 (US).</p> <p>(74) Common Representative: MERCK & CO., INC.; 126 East Lincoln Avenue, Rahway, NJ 07065-0907 (US).</p>		<p>(81) Designated States: CA, JP, US, European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).</p> <p>Published <i>Without international search report and to be republished upon receipt of that report.</i></p>
<p>(54) Title: DNA MOLECULES ENCODING HUMAN ENDOTHELIN CONVERTING ENZYME 3</p> <div style="display: flex; justify-content: space-between;"> <div style="width: 48%;"> <p>Met Glu Pro Pro Tyr Ser Leu Thr Ala His Tyr Asp Glu Phe Gln Glu Val Lys Tyr Val Ser Arg Cys Gly Ala Gly Gly Ala Arg Gly Ala Ser Leu Pro Pro Gly Phe Pro Leu Gly Ala Ala Arg Ser Ala Thr Gly Ala Arg Ser Gly Leu Pro Arg Trp Asn Arg Arg Glu Val Cys Leu Leu Ser Gly Leu Val Phe Ala Ala Gly Leu Cys Ala Ile Leu Ala Ala Met Leu Ala Leu Lys Tyr Leu Gly Pro Val Ala Ala Gly Gly Gly Ala Cys Pro Glu Gly Cys Pro Glu Arg Lys Ala Phe Ala Arg Ala Ala Arg Phe Leu Ala Ala Asn Leu Asp Ala Ser Ile Asp Pro Cys Gln Asp Phe Tyr Ser Phe Ala Cys Gly Gly Trp Leu Arg Arg, His Ala Ile Pro Asp Asp Lys Leu Thr Tyr Gly Thr Ile Ala Ala Ile Gly Glu Gln Asn Glu Glu Arg Leu Arg Arg Leu Leu Ala Arg Pro Gly Gly Gly Pro Gly Gly Ala Ala Gln Arg Lys Val Arg Ala Phe Phe Arg Ser Cys Leu Asp Met Arg Glu Ile Glu Arg Leu Gly Pro Arg Pro Met Leu Glu Val Ile Glu Asp Cys Gly Gly Trp Asp Leu Gly Gly Ala Glu Glu Arg Pro Gly Val Ala Ala Arg Trp Asp Leu Asn Arg Leu Leu Tyr Lys Ala Gln Gly Val Tyr Ser Ala Ala Ala Leu Phe Ser Leu Thr Val Ser Leu Asp Arg Asn Ser Ser Arg Tyr Val Ile Arg Ile Asp Gln Asp Gly Leu Thr Leu Pro Glu Arg Thr Leu Tyr Leu Ala Gln Asp Glu Asp Ser Glu Lys Ile Leu Ala Ala Tyr Arg Val Phe Met Glu Arg Val Leu Ser Leu Leu Gly Ala Asp Ala Val Glu Gln Lys Ala Gln Glu Ile Leu Gln Val Glu Gln Gln Leu Ala Asn Ile Thr Val Ser Glu Tyr Asp Asp Leu Arg Arg Asp Val Ser Ser Met Tyr Asn Lys Val Thr Leu Gly Gln Leu Gln Lys Ile Thr Pro His Leu Arg Trp Lys Trp Leu Leu Asp Gln Ile Phe Gln Glu Asp Phe Ser Glu Glu Glu Glu Val Val Leu Leu Ala Thr Asp Tyr Met Gln Gln Val Ser Gln Leu Ile Arg Ser Thr Pro His Arg Val Leu His Asn Tyr Leu Val Trp Arg Val Val Val Val Leu Ser Glu His Leu Ser Pro Pro</p> </div> <div style="width: 48%;"> <p>Phe Arg Glu Ala Leu His Glu Leu Ala Gln Glu Met Glu Gly Ser Asp Lys Pro Gln Glu Leu Ala Arg Val Cys Leu Gly Gln Ala Asn Arg His Phe Gly Met Ala Leu Gly Ala Leu Phe Val His Glu His Phe Ser Ala Ala Ser Lys Ala Lys Val Gln Gln Leu Val Glu Asp Ile Lys Tyr Ile Leu Gly Gln Arg Leu Glu Glu Leu Asp Trp Met Asp Ala Glu Thr Arg Ala Ala Ala Arg Ala Lys Leu Gln Tyr Met Met Val Met Val Gly Tyr Pro Asp Phe Leu Leu Lys Pro Asp Ala Val Asp Lys Glu Tyr Glu Phe Glu Val His Glu Lys Thr Tyr Phe Lys Asn Ile Leu Asn Ser Ile Arg Phe Ser Ile Gln Leu Ser Val Lys Lys Ile Arg Gln Glu Val Asp Lys Ser Thr Trp Leu Leu Pro Pro Gln Ala Leu Asn Ala Tyr Tyr Leu Pro Asn Lys Asn Gln Met Val Phe Pro Ala Gly Ile Leu Gln Pro Thr Leu Tyr Asp Pro Asp Phe Pro Gln Ser Leu Asn Tyr Gly Gly Ile Gly Thr Ile Ile Gly His Glu Leu Thr His Gly Tyr Asp Asp Trp Gly Gly Gln Tyr Asp Arg Ser Gly Asn Leu Leu His Trp Trp Thr Glu Ala Ser Tyr Ser Arg Phe Leu Arg Lys Ala Glu Cys Ile Val Arg Leu Tyr Asp Asn Phe Thr Val Tyr Asn Gln Arg Val Asn Gly Lys His Thr Leu Gly Glu Asn Ile Ala Asp Met Gly Gly Leu Lys Leu Ala Tyr His Ala Tyr Gln Lys Trp Val Arg Glu His Gly Pro Glu His Pro Leu Pro Arg Leu Lys Tyr Thr His Asp Gln Leu Phe Phe Ile Ala Phe Ala Gln Asn Trp Cys Ile Lys Arg Arg Ser Gln Ser Ile Tyr Leu Gln Val Leu Thr Asp Lys His Ala Pro Glu His Tyr Arg Val Leu Gly Ser Val Ser Gln Phe Glu Glu Phe Gly Arg Ala Phe His Cys Pro Lys Asp Ser Pro Met Asn Pro Ala His Lys Cys Ser Val Trp (SEQ ID NO:2)</p> </div> </div> <p>(57) Abstract</p> <p>The present invention relates to human DNA molecules encoding the endothelin converting enzyme-3(ECE-3)protein, recombinant vectors comprising DNA molecules encoding ECE-3, recombinant host cells which contain a recombinant vector encoding ECE-3, the ECE-3 protein encoded by the DNA molecule, and methods of identifying selective agonists and antagonists of ECE-3.</p>		

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TITLE OF THE INVENTION

5 DNA MOLECULES ENCODING HUMAN ENDOTHELIN
CONVERTING ENZYME 3

CROSS-REFERENCE TO RELATED APPLICATIONS

10 Not Applicable

STATEMENT REGARDING FEDERALLY-SPONSORED R&D

15 Not Applicable

REFERENCE TO MICROFICHE APPENDIX

20 Not Applicable

FIELD OF THE INVENTION

The present invention relates to human DNA molecules encoding endothelin converting enzyme 3 (ECE-3), a membrane bound metalloprotease which proteolytically cleaves endothelin precursors to their active form, recombinant vectors comprising DNA molecules encoding ECE-3, recombinant host cells which contain a recombinant vector encoding ECE-3, the ECE-3 protein encoded by the DNA molecule, and methods of identifying selective modulators of ECE-3.

25

30 BACKGROUND OF THE INVENTION

Endothelins constitute a small family of 21 amino acid peptides that possess a various biological activities. These peptides are characterized by cysteine residues at positions 1, 3, 11 and 15. Endothelin-1 (ET-1) was the first to be disclosed and has been shown to be a potent endothelium-derived vasoconstrictor (Yanagisawa

et al., 1988, *Nature* 332: 411-415). The three known members of the endothelin family: ET-1, Endothelin-2 (ET-2) and Endothelin-3 (ET-3)] are produced in various tissues and are known to interact with two distinct G-protein coupled receptors, ETA and ETB (Elshourbagy et al., 1993, *J. Biol. Chem.* 268: 3873-3879), which are
5 expressed in various cell types.

The endothelins are produced from large prepropeptides of approximately 200 amino acids. These precursors are initially cleaved into inactive 38-41 amino acid intermediates referred to as big ET-1, big ET-2 and big ET-3, respectively (Seidah, et al., 1993, *Ann. NY Acad. Sci.* 680: 135-146). The carboxy-
10 terminal portion of the big ETs are then proteolytically cleaved at a conserved Trp21-Val/Ile22 juncture to produce the active endothelin peptide (i.e., ET-1, ET-2 or ET-3, respectively). The enzymes responsible for proteolytic cleavage of the big ETs to produce active endothelins are referred to as endothelin-converting enzymes (ECEs). To date, two ECEs have been disclosed, endothelin-converting enzyme 1 (ECE-1) and
15 endothelin-converting enzyme 2 (ECE-2).

U.S. Patent No. 5,231,166, issued to Masaki et al on July 27, 1993, discloses and claims endothelin- 2.

U.S. Patent No. 5,294,569, issued to Masaki et al on March 15, 1994, discloses and claims DNA molecules which encode endothelin- 2.

20 U.S. Patent No. 5,548,061, issued to Masaki et al on August 20, 1996, discloses and claims endothelin- 3.

U.S. Patent No. 5,811,263 issued to Masaki et al on September 22, 1998, discloses and claims DNA molecules which encode endothelin- 3.

25 U.S. Patent No. 5,688,640, issued to Yanagisawa on November 18, 1997, discloses and claims methods of screening for modulators of ECE-1 utilizing bovine ECE-1.

Xu et al (1994, *Cell* 78: 473-485) disclose a cDNA encoding bovine ECE-1 and the concomitant amino acid sequence of bovine ECE-1.

30 U.S. Patent No. 5,736,376, issued to Yanagisawa on April 7, 1998, discloses and claims compositions which comprise bovine ECE-2.

Emoto and Yanagisawa (1995, *J. Biol. Chem.* 270 (25): 15262-15268) disclose a cDNA encoding bovine ECE-2 and the concomitant amino acid sequence of bovine ECE-2.

There is a body of work showing that specific antagonists of endothelin may play crucial roles in vascular disease models (e.g., see Ohlstein, et al., 1994, *Proc. Natl. Acad. Sci.* 91: 8052-8056; Clozel et al., 1993, *Nature* 365: 759-761; Giaid et al., 1993, *N. Engl. J. Med.* 328:1732-1740; Douglas et al., 1994, *Trends Pharmacol. Sci* 15: 313-316). Such modulators of endothelin levels may be useful to treat diseases such as hypertension, atherosclerosis and vascular restenosis, myocardial ischemia, cerebral vasospasm and subarachnoid hemorrhage, congestive heart failure, diabetes, endotoxic shock, migraine, possibly Raynaud's phenomenon (for a review, see Ohlstein et al., *Functions Mediated by Peripheral Endothelin Receptors: in Endothelin Receptors: From the Gene to the Heart*, @ Chapter 6, pp. 109-185; CRC Press, Boca Raton, FL, 1995) as well as pulmonary diseases such as asthma, pulmonary hypertension and adult respiratory distress syndrome (see also, Jorkasky et al., *The Role of Endothelin in Human Disease: Implications and Potential Therapeutic Intervention: in Endothelin Receptors: From the Gene to the Heart*, @ Chapter 8, pp. 215-271; CRC Press, Boca Raton, FL, 1995).

Despite the identification of ECEs as described above, it would be advantageous to identify additional ECEs, especially novel human ECEs, that are active in the cascade of events involving human endothelins and endothelin receptors. As pointed out by Xu et al (id.), bovine ECE-1 and bovine ECE-2 possess a strong preference for the big ET-1 substrate over the big ET-2 or big ET-3, showing that additional ECEs may exist and may have difference substrate specificity. The present invention addresses and meets these needs by disclosing an isolated nucleic acid fragment which expresses a form of human ECE-3, recombinant vectors which house this nucleic acid fragment, recombinant host cells which expresses human ECE-3 and/or a biologically active equivalent, and method of using DNA molecules encoding human ECE-3 and/or recombinant human ECE-3 protein to select modulators of ECE-3 and other ECE forms which in turn directly effect endothelin production and endothelin receptor function.

SUMMARY OF THE INVENTION

The present invention relates to an isolated or purified nucleic acid molecule (polynucleotide) which encodes a novel human endothelin converting enzyme, ECE-3. The nucleic acid molecules of the present invention are substantially free from other nucleic acids.

The present invention relates to an isolated nucleic acid molecule (polynucleotide) which encodes mRNA which expresses a novel novel human endothelin converting enzyme, ECE-3, this DNA molecule comprising the nucleotide sequence disclosed herein as SEQ ID NO:1.

5 The present invention also relates to biologically active fragments or mutants of SEQ ID NO:1 which encodes mRNA expressing a novel human endothelin converting enzyme, ECE-3. Any such biologically active fragment and/or mutant will encode either a protein or protein fragment which at least substantially mimics the pharmacological properties of a wild-type ECE-3 protein, including but not limited to
10 the ECE-3 protein as set forth in SEQ ID NO:2. Any such polynucleotide includes but is not necessarily limited to nucleotide substitutions, deletions, additions, amino-terminal truncations and carboxy-terminal truncations such that these mutations encode mRNA which express a protein or protein fragment of diagnostic, therapeutic or prophylactic use and would be useful for screening for agonists and/or antagonists
15 for ECE-3 function.

A preferred aspect of this portion of the present invention is disclosed in Figure 1A-B and Figure 4A-F, a human cDNA molecule (SEQ ID NO:1) encoding a novel ECE-3 protein.

20 The isolated nucleic acid molecules of the present invention may include a deoxyribonucleic acid molecule (DNA), such as genomic DNA and complementary DNA (cDNA), which may be single (coding or noncoding strand) or double stranded, as well as synthetic DNA, such as a synthesized, single stranded polynucleotide. The isolated nucleic acid molecule of the present invention may also include a ribonucleic acid molecule (RNA).

25 The present invention also relates to recombinant vectors and recombinant hosts, both prokaryotic and eukaryotic, which contain the substantially purified nucleic acid molecules disclosed throughout this specification.

30 The present invention also relates to subcellular membrane fractions of the recombinant host cells (both prokaryotic and eukaryotic as well as both stably and transiently transformed cells) which contain the proteins encoded by the nucleic acids of the present invention. These subcellular membrane fractions will comprise either wild-type or mutant forms of human ECE-3 proteins at levels substantially above endogenous levels and hence will be useful in various assays described throughout this specification. The preferred eukaryotic subcellular membrane locations for the

ECEs of the present invention include the cell membrane and the intracellular Golgi membrane.

The present invention also relates to a substantially purified form of the human ECE-3 protein, which comprises the amino acid sequence disclosed in Figure 2A-B and Figure 4A-F and set forth as SEQ ID NO:2.

A preferred aspect of this portion of the present invention is human ECE-3, which consists of the amino acid sequence as set forth in SEQ ID NO:2 and Figure 2A-B and Figure 4A-F.

The present invention also relates to biologically active fragments and/or mutants of human ECE-3, comprising the amino acid sequence as set forth in SEQ ID NO:2, including but not necessarily limited to amino acid substitutions, deletions, additions, amino terminal truncations and carboxy-terminal truncations such that these mutations provide for proteins or protein fragments of diagnostic, therapeutic or prophylactic use and would be useful for screening for selective modulators, including but not limited to agonists and/or antagonists for ECE-3 function.

A preferred aspect of the present invention is disclosed in Figure 2A-B and Figure 4A-F and is set forth as SEQ ID NO:2, the amino acid sequence of the novel human ECE-3. Endothelin converting enzyme-3 is a novel member of ECE family of enzymes involved in the cleavage of big ET precursors to the active endothelin forms, ET-1, ET-2 and ET-3. The isolation, characterization and disclosure of a human form of a novel member of the ECE family will allow for more sophisticated methods of identifying selective modulators of the endothelin pathway in humans. The potential disease targets are exhaustive [e.g., see Xu et al (1994, *Cell* 78: 473-485) for a listing of pertinent literature], with the involvement of endothelins in systemic hypertension being an especially preferred area of concentration. Therefore, while other endothelin-converting enzymes have been isolated in the past, they have not accounted for all the production or actions of endothelin. The advantage of this invention is that it identifies a new member of the family of biosynthetic enzymes responsible for endothelin production, and thus represents a novel potential drug target. The products and method of the present invention will therefore also be useful for the study of endothelin production, metabolism, and biology as well as being useful in a potential compound screen for inhibitors of the

enzyme that may be therapeutic for various diseases mentioned herein, including but in no way limited to hypertension, vasospasm, or other vascular disorders.

The present invention also relates to polyclonal and monoclonal antibodies raised in response to either the human form of ECE-3, or a biologically
5 active fragment thereof.

The present invention also relates to isolated nucleic acid molecules which are fusion constructions expressing fusion proteins useful in assays to identify compounds which modulate wild-type vertebrate ECE-3. A preferred aspect of this portion of the invention includes, but is not limited to, glutathione S-transferase
10 (GST)-ECE-3 fusion constructs which include, but are not limited to, either the intracellular or intraluminal domain of human ECE-3 as an in-frame fusion at the carboxy terminus of the GST gene, or the extracellular and transmembrane ligand binding domain of ECE-3 fused to the amino terminus of GST, or the extracellular and transmembrane domain of ECE-3 fused to an immunoglobulin gene by methods
15 known to one of ordinary skill in the art. Soluble recombinant GST-ECE-3 fusion proteins may be expressed in various expression systems, including *Spodoptera frugiperda* (Sf21) insect cells (Invitrogen) using a baculovirus expression vector (pAcG2T, Pharmingen). Such fusion constructs may also be useful in the generation of antibodies against ECE-3.

20 Therefore, the present invention relates to methods of expressing the human ECE-3 protein and biological equivalents disclosed herein, assays employing these gene products, recombinant host cells which comprise DNA constructs which express these proteins, and compounds identified through these assays which act as agonists or antagonists of ECE-3 activity or of another component of the endothelin
25 pathway.

It is an object of the present invention to provide an isolated nucleic acid molecule (e.g., SEQ ID NO:1) which encodes a novel form of human ECE-3, or human ECE-3 fragments, mutants or derivatives of SEQ ID NO:2. Any such polynucleotide includes but is not necessarily limited to nucleotide substitutions,
30 deletions, additions, amino-terminal truncations and carboxy-terminal truncations such that these mutations encode mRNA which express a protein or protein fragment of diagnostic, therapeutic or prophylactic use and would be useful for screening for selective modulators for vertebrate ECE-3 function.

It is a further object of the present invention to provide the human ECE-3 proteins or protein fragments encoded by the nucleic acid molecules referred to in the preceding paragraph.

It is a further object of the present invention to provide recombinant
5 vectors and recombinant host cells which comprise a nucleic acid sequence encoding human ECE-3 or a biological equivalent thereof.

It is an object of the present invention to provide a substantially purified form of the human ECE-3 protein, as set forth in SEQ ID NO:2.

It is an object of the present invention to provide for biologically active
10 fragments and/or mutants of the human ECE-3 protein, such as set forth in SEQ ID NO:2, including but not necessarily limited to amino acid substitutions, deletions, additions, amino terminal truncations and carboxy-terminal truncations such that these mutations provide for proteins or protein fragments of diagnostic, therapeutic and/or prophylactic use.

It is further an object of the present invention to provide for
15 substantially purified subcellular fractions which comprise human ECE-3, especially subcellular fractions obtained from a host cell transfected or transformed with a DNA vector comprising a nucleotide sequence which encodes a protein which comprises the amino acid as set forth in SEQ ID NO:2 and Figure 2A-B and Figure 4A-F.

It is also an object of the present invention to provide for ECE-3-based
20 in-frame fusion constructions, methods of expressing these fusion constructs, biological equivalents disclosed herein, related assays, recombinant cells expressing these constructs, and agonistic and/or antagonistic compounds identified through the use of the nucleic acid encoding vertebrate, mammalian and/or human ECE-3 protein
25 as well as the expressed protein itself.

It is also an object of the present invention to use ECE-3 or membrane preparations containing ECE-3 or a biological equivalent to screen for modulators, preferably selective modulators, of ECE-3 activity. Any such compound may be useful in a diagnostic, therapeutic and/or prophylactic indications for such disease
30 states as hypertension, atherosclerosis and vascular restenosis, myocardial ischemia, cerebral vasospasm, cerebral ischemia and subarachnoid hemorrhage, congestive heart failure, diabetes, benign prostatic hypertrophy, erectile dysfunction, renal disease and dysfunction, endotoxic shock, migraine, possibly Raynaud's phenomenon, as well

as pulmonary diseases such as asthma, pulmonary hypertension and adult respiratory distress syndrome.

As used herein, "substantially free from other nucleic acids" means at least 90%, preferably 95%, more preferably 99%, and even more preferably 99.9%, free of other nucleic acids. Thus, an ECE-3 DNA preparation that is substantially free from other nucleic acids will contain, as a percent of its total nucleic acid, no more than 10%, preferably no more than 5%, more preferably no more than 1%, and even more preferably no more than 0.1%, of non-ECE-3 nucleic acids. Whether a given ECE-3 DNA preparation is substantially free from other nucleic acids can be determined by such conventional techniques of assessing nucleic acid purity as, *e.g.*, agarose gel electrophoresis combined with appropriate staining methods, *e.g.*, ethidium bromide staining, or by sequencing.

As used herein, "substantially free from other proteins" or "substantially purified" means at least 90%, preferably 95%, more preferably 99%, and even more preferably 99.9%, free of other proteins. Thus, an ECE-3 protein preparation that is substantially free from other proteins will contain, as a percent of its total protein, no more than 10%, preferably no more than 5%, more preferably no more than 1%, and even more preferably no more than 0.1%, of non-ECE-3 proteins. Whether a given ECE-3 protein preparation is substantially free from other proteins can be determined by such conventional techniques of assessing protein purity as, *e.g.*, sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) combined with appropriate detection methods, *e.g.*, silver staining or immunoblotting. As used interchangeably with the terms "substantially free from other proteins" or "substantially purified", the terms "isolated ECE-3 protein" or "purified ECE-3 protein" also refer to ECE-3 protein that has been isolated from a natural source. Use of the term "isolated" or "purified" indicates that ECE-3 protein has been removed from its normal cellular environment. Thus, an isolated ECE-3 protein may be in a cell-free solution or placed in a different cellular environment from that in which it occurs naturally. The term isolated does not imply that an isolated ECE-3 protein is the only protein present, but instead means that an isolated ECE-3 protein is substantially free of other proteins and non-amino acid material (*e.g.*, nucleic acids, lipids, carbohydrates) naturally associated with the ECE-3 protein *in vivo*. Thus, an ECE-3 protein that is expressed in a prokaryotic or eukaryotic cell which do not naturally (*i.e.*, without human intervention) express it through recombinant means is

an "isolated ECE-3 protein." As noted above, an ECE-3 protein preparation that is an isolated or purified ECE-3 protein will be substantially free from other proteins will contain, as a percent of its total protein, no more than 10%, preferably no more than 5%, more preferably no more than 1%, and even more preferably no more than 0.1%, of non-ECE-3 proteins.

As used interchangeably herein, "functional equivalent" or "biologically active equivalent" means a protein which does not have exactly the same amino acid sequence as naturally occurring ECE-3, due to alternative splicing, deletions, mutations, substitutions, or additions, but retains substantially the same biological activity as ECE-3. Such functional equivalents will have significant amino acid sequence identity with naturally occurring ECE-3 and genes and cDNA encoding such functional equivalents can be detected by reduced stringency hybridization with a DNA sequence encoding naturally occurring ECE-3. For the purposes of this invention, naturally occurring ECE-3 has the amino acid sequence shown as SEQ ID NO:2 and is encoded by SEQ ID NO:1. A nucleic acid encoding a functional equivalent has at least about 50% identity at the nucleotide level to SEQ ID NO:1.

As used herein, "a conservative amino acid substitution" refers to the replacement of one amino acid residue by another, chemically similar, amino acid residue. Examples of such conservative substitutions are: substitution of one hydrophobic residue (isoleucine, leucine, valine, or methionine) for another; substitution of one polar residue for another polar residue of the same charge (e.g., arginine for lysine; glutamic acid for aspartic acid).

As used herein, "ECE" refers to -- endothelin converting enzyme --.
As used herein, "ECE-1" refers to -- endothelin converting enzyme-1 --.

As used herein, "ECE-2" refers to -- endothelin converting enzyme-2 --.

As used herein, "ECE-3" refers to -- endothelin converting enzyme-3 --.

As used herein, the term "mammalian host" will refer to any mammal, including a human being.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1A-B show the nucleotide sequence which encodes human ECE-3, as set forth in SEQ ID NO:1.

Figure 2A-B show the amino acid sequence of human ECE-3, as set forth in SEQ ID NO:2.

Figure 3A-D show an autoradiograph of a Northern blot of tissue-specific human mRNA. This Northern analysis show the human ECE-3 gene to be expressed in medulla oblongata and ovary at a high level; putamen, spinal cord, caudate nucleus, substantia nigra, thalamus, and testis at a medium level; and amygdala, corpus callosum, hippocampus, whole brain, subthalamic nucleus, cerebellum, cerebral cortex, occipital pole, frontal lobe, temporal lobe, thymus, prostate, skeletal muscle, kidney, pancreas and heart at a low level.

Figure 4A-F show the coding (SEQ ID NO:1), and anticoding (SEQ ID NO:22) DNA sequence as well as the open reading frame and amino acid sequence (SEQ ID NO:2) human ECE-3.

DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to an isolated nucleic acid molecule (polynucleotide) which encodes a novel human endothelin converting enzyme, endothelin converting enzyme-3 (ECE-3). The nucleic acid molecules of the present invention are substantially free from other nucleic acids. For most cloning purposes, DNA is a preferred nucleic acid.

The present invention relates to an isolated nucleic acid molecule (polynucleotide) which encodes mRNA which expresses a novel human ECE-3, this DNA molecule comprising the nucleotide sequence disclosed herein as SEQ ID NO:1, shown herein as follows:

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GGCGGCGGGC GCTGGGAGAC ACCGGACGCC CGCTCGGCTG CGCTGCGGCT CAGGCCCCCG
CTCGGGCCCCG ACCCGCTCGG TCACCGCCGG CTCGGGCGCG CACCTGCCGG CTGCGGCCCC
AGGGCCATGC GGAGGCCAC GAGGAGGCCG GCGGCCACGC GCATCCCGTA GCCCAGGTGG
30 CCCAGGTCTG CACCGCGGCG GCCTCGGCGC CATGGAGCCC CCGTATTTCG TGACGGCGCA
CTACGATGAG TTCCAAGAGG TCAAGTACGT GAGCCGCTGC GCGCGGGGG GCGCGCGCGG
GGCCTCCCTG CCCCCGGGCT TCCCGTTGGG CGCTGCCCCG AGCGCCACCG GGGCCCGGTC
CGGGCTGCCG CGCTGGAACC GCGCGGAGGT GTGCCTGCTG TCGGGGCTGG TGTTCGCCCG
CGGCCTCTGC GCCATTCTGG CGGCTATGCT GGCCCTCAAG TACCTGGGCC CGGTGCGGGC

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CGGCGGCGGC GCCTGTCCCG AGGGCTGCCC TGAGCGCAAG GCCTTCGCGC GCGCCGCTCG
CTTCCTGGCC GCCAACCTGG ACGCCAGCAT CGACCCATGC CAGGACTTCT ACTCGTTCGC
CTGCGGCGGT TGGCTGCGGC GCCACGCCAT CCCCAGCGAC AAGCTCACCT ATGGCACCAT
CGCGGCCATC GGCGAGCAAA ACGAGGAGCG CCTACGGCGC CTGCTGGCGC GGCCCGGGGG
5 TGGGCCTGGC GGCGCGGCCC AGCGCAAGGT GCGCGCCTTC TTCCGCTCGT GCCTCGACAT
GCGCGAGATC GAGCGACTGG GCCCGCGACC CATGCTAGAG GTCATCGAGG ACTGCGGGGG
CTGGGACCTG GGCGGCGCGG AGGAGCGTCC GGGGGTCGCG GCGCGATGGG ACCTCAACCG
GCTGCTGTAC AAGGCGCAGG GCGTGTACAG CGCCGCCGCG CTCTTCTCGC TCACGGTCAG
CCTGGACGAC AGGAACTCCT CGCGCTACGT CATCCGATT GACCAGGATG GGCTCACCT
10 GCCAGAGAGG ACCCTGTACC TCGCTCAGGA TGAGGACAGT GAGAAGATCC TGGCAGCATA
CAGGGTGTTC ATGGAGCGAG TGCTCAGCCT CCTGGGTGCA GACGCTGTGG AACAGAAGGC
CCAAGAGATC CTGCAAGTGG AGCAGCAGCT GGCCAACATC ACTGTGTCAG AGTATGACGA
CCTACGGCGA GATGTCAGCT CCATGTACAA CAAGGTGACG CTGGGGCAGC TGCAGAAGAT
CACCCCCAC TTGCGGTGGA AGTGGCTGCT AGACCAGATC TTCCAGGAGG ACTTCTCAGA
15 GGAAGAGGAG GTGGTGCTGC TGGCGACAGA CTACATGCAG CAGGTGTCGC AGCTCATCCG
CTCCACACCC CACCGGGTCC TGCACAATA CCTGGTGTGG CGCGTGGTGG TGGTCCTGAG
TGAACACCTG TCCCCGCCAT TCCGTGAGGC ACTGCACGAG CTGGCACAGG AGATGGAGGG
CAGCGACAAG CCACAGGAGC TGGCCCCGGT CTGCTTGGGC CAGGCCAATC GCCACTTTGG
CATGGCGCTT GGCGCCCTCT TTGTACATGA GCACTTCTCA GCTGCCAGCA AAGCCAAGGT
20 GCAGCAGCTA GTGGAAGACA TCAAGTACAT CCTGGGCCAG CGCCTGGAGG AGCTGGACTG
GATGGACGCC GAGACCAGGG CTGCTGCTCG GGCCAAGCTC CAGTACATGA TGGTGATGGT
CGGCTACCCG GACTTCCTGC TGAAACCCGA TGCTGTGGAC AAGGAGTATG AGTTTGAGGT
CCATGAGAAG ACCTACTTCA AGAACATCTT GAACAGCATC CGCTTCAGCA TCCAGCTCTC
AGTTAAGAAG ATTTCGGCAGG AGGTGGACAA GTCCACGTGG CTGCTCCCCC CACAGGCGCT
25 CAATGCCTAC TATCTACCCA ACAAGAACCA GATGGTGTTC CCCGCGGGCA TCCTGCAGCC
CACCTGTAC GACCCTGACT TCCCACAGTC TCTCAACTAC GGGGGCATCG GCACCATCAT
TGGACATGAG CTGACCCACG GCTACGACGA CTGGGGGGGC CAGTATGACC GCTCAGGGAA
CCTGCTGCAC TGGTGGACGG AGGCCTCCTA CAGCCGCTTC CTGCGAAAGG CTGAGTGCAT
CGTCCGTCTC TATGACAACT TCACTGTCTA CAACCAGCGG GTGAACGGGA AACACACGCT
30 TGGGGAGAAC ATCGCAGATA TGGGCGGCCT CAAGCTGGCC TACCACGCCT ATCAGAAGTG
GGTGCGGGAG CACGGCCCAG AGCACCCACT TCCCCGGCTC AAGTACACAC ATGACCAGCT
CTTCTTCATT GCCTTTGCCC AGAACTGGTG CATCAAGCGG CGGTCGCAGT CCATCTACCT
GCAGGTGCTG ACTGACAAGC ATGCCCTGA GCACTACAGG GTGCTGGGCA GTGTGTCCCA
GTTTGAGGAG TTTGGCCGGG CTTTCCACTG TCCCAAGGAC TCACCCATGA ACCCTGCCCA

CAAGTGTTCC GTGTGGTGAG CCTGGCTGCC CGCCTGCACG CCCCCACTGC CCCCGCACGA
 ATCACCTCCT GCTGGCTACC GGGGCAGGCA TGCACCCGGT GCCAGCCCCG CTCTGGGCAC
 CACCTGCCTT CCAGCCCCTC CAGGACCCGG TCCCCCTGCT GCCCCTCACT TCAGGAGGGG
 CCTGGAGCAG GGTGAGGCTG GACTTTGGGG GGCTGTGAGG GAAATATACT GGGGTCCCCA
 5 GATTCTGCTC TAAGGGGGCC AGACCCTCTG CCAGGCTGGA TTGTACGGGC CCCACCTTCG
 CTGTGTTCTT GCTGCAAAGT CTGGTCAATA AATCACTGCA CTGTTAAAAA AAAAAAAAAA
 AAAAAATTCC TCG (SEQ ID NO:1).

The above-exemplified isolated DNA molecule, shown in Figure 1A-B and Figure 4A-F and set forth as SEQ ID NO:1, contains 2894 nucleotides. This
 10 DNA molecule contains an open reading frame from nucleotide 212 (initiating Met from nt 212-214) to nucleotide 2536, with a "TGA" termination codon from nucleotides 2537-2539. A Kozak sequence (GGCGCCATGG [contained from nt 206-215 of SEQ ID NO:1]) is present and a polyA+ site is evident from nt 2866-2886 of SEQ ID NO:1. This open reading frame encodes a preferred form of the present
 15 invention, a human ECE-3 protein. The ECE-3 protein contains an open reading frame of 775 amino acids in length, as shown in Figure 2A-B and Figure 4A-F and as set forth in SEQ ID NO:2. Radiation hybrid mapping assigns this gene to chromosome 2q37, in a region that has not been linked to any human disease that might logically be due to ECE mutation. Northern analysis show the gene to be
 20 expressed in medulla and ovary at a high level; putamen, spinal cord, testis, caudate nucleus, substantia nigra and thalamus at a medium level; and amygdala, corpus callosum, hippocampus, whole brain, subthalamic nucleus, cerebellum, cerebral cortex, occipital pole, frontal lobe, temporal lobe, thymus, prostate, skeletal muscle, kidney, pancreas and heart at a low level (Figure 3A-3D).

25 The full length cDNA encoding ECE-3 was isolated by initially searching a public EST database, wherein an EST corresponding to a third member of the endothelin family was found, and a full-length sequence was isolated by EST sequencing and RACE (Rapid Amplification of cDNA Ends). A unigene search looking for endothelin converting enzyme hits index class Hs.26880 which consists of
 30 3 ESTs and is annotated as being 44% similar to the rat ECE-1. The three ESTs represent 2 Image clones (AA523527, [R61440, R61395]). R61440 is a 5' EST 606 bp long (SEQ ID NO: 3) which hits KIAA0604 with 60% similarity over only a portion of the full length EST (167/276 bp). No similar ESTs were found during this search of the public database. The two 3' EST sequences (SEQ ID NOs: 4 and 5) are

identical to each other and to no other EST. The nucleotide sequence of each EST (SEQ ID NOs: 3-5) are disclosed in Example Section 1 of this specification as well as from the National Center for Biotechnology Information (NCBI) homepage at <http://www.ncbi.nlm.nih.gov/>.

5 The present invention also relates to biologically active fragments or mutants of SEQ ID NO:1 which encodes mRNA expressing ECE-3. Any such biologically active fragment and/or mutant will encode either a protein or protein fragment which at least substantially mimics the enzymatic properties of human ECE-3 protein, including but not limited to the human ECE-3 protein as set forth in SEQ ID
10 NO:2. Any such polynucleotide includes but is not necessarily limited to nucleotide substitutions, deletions, additions, amino-terminal truncations and carboxy-terminal truncations such that these mutations encode mRNA which express a protein or protein fragment of diagnostic, therapeutic or prophylactic use and would be useful for screening for agonists and/or antagonists for ECE-3 function and/or of modulators
15 of other components of the endothelin receptor pathway.

A preferred aspect of this portion of the present invention is disclosed in Figure 1A-B, a cDNA molecule encoding human ECE-3 (SEQ ID NO:1).

The isolated nucleic acid molecules of the present invention may include a deoxyribonucleic acid molecule (DNA), such as genomic DNA and
20 complementary DNA (cDNA), which may be single (coding or noncoding strand) or double stranded, as well as synthetic DNA, such as a synthesized, single stranded polynucleotide. The isolated nucleic acid molecule of the present invention may also include a ribonucleic acid molecule (RNA).

The degeneracy of the genetic code is such that, for all but two
25 amino acids; more than a single codon encodes a particular amino acid. This allows for the construction of synthetic DNA that encodes the ECE-3 protein where the nucleotide sequence of the synthetic DNA differs significantly from the nucleotide sequence of SEQ ID NO:1, but still encodes the same ECE-3 protein as SEQ ID NO:1. Such synthetic DNAs are intended to be within the scope of the
30 present invention. If it is desired to express such synthetic DNAs in a particular host cell or organism, the codon usage of such synthetic DNAs can be adjusted to reflect the codon usage of that particular host, thus leading to higher levels of expression of ECE-3 protein in the host. In other words, this redundancy in the various codons which code for specific amino acids is within the scope of the

present invention. Therefore, this invention is also directed to those DNA sequences which encode RNA comprising alternative codons which code for the eventual translation of the identical amino acid, as shown below:

- A=Ala=Alanine: codons GCA, GCC, GCG, GCU
- 5 C=Cys=Cysteine: codons UGC, UGU
- D=Asp=Aspartic acid: codons GAC, GAU
- E=Glu=Glutamic acid: codons GAA, GAG
- F=Phe=Phenylalanine: codons UUC, UUU
- G=Gly=Glycine: codons GGA, GGC, GGG, GGU
- 10 H=His =Histidine: codons CAC, CAU
- I=Ile =Isoleucine: codons AUA, AUC, AUU
- K=Lys=Lysine: codons AAA, AAG
- L=Leu=Leucine: codons UUA, UUG, CUA, CUC, CUG, CUU
- M=Met=Methionine: codon AUG
- 15 N=Asp=Asparagine: codons AAC, AAU
- P=Pro=Proline: codons CCA, CCC, CCG, CCU
- Q=Gln=Glutamine: codons CAA, CAG
- R=Arg=Arginine: codons AGA, AGG, CGA, CGC, CGG, CGU
- S=Ser=Serine: codons AGC, AGU, UCA, UCC, UCG, UCU
- 20 T=Thr=Threonine: codons ACA, ACC, ACG, ACU
- V=Val=Valine: codons GUA, GUC, GUG, GUU
- W=Trp=Tryptophan: codon UGG
- Y=Tyr=Tyrosine: codons UAC, UAU

Therefore, the present invention discloses codon redundancy which may result in
 25 differing DNA molecules expressing an identical protein. For purposes of this specification, a sequence bearing one or more replaced codons will be defined as a degenerate variation. Also included within the scope of this invention are mutations either in the DNA sequence or the translated protein which do not substantially alter the ultimate physical properties of the expressed protein. For
 30 example, substitution of valine for leucine, arginine for lysine, or asparagine for glutamine may not cause a change in functionality of the polypeptide.

It is known that DNA sequences coding for a peptide may be altered so as to code for a peptide having properties that are different than those of the naturally occurring peptide. Methods of altering the DNA sequences include

but are not limited to site directed mutagenesis. Examples of altered properties include but are not limited to changes in the affinity of an enzyme for a substrate or a receptor for a ligand.

The present invention also relates to recombinant vectors and
5 recombinant hosts, both prokaryotic and eukaryotic, which contain the substantially purified nucleic acid molecules disclosed throughout this specification. The nucleic acid molecules of the present invention encoding ECE-3, in whole or in part, can be linked with other DNA molecules, i.e., DNA molecules to which the human ECE-3 are not naturally linked, to form "recombinant DNA molecules" which encode ECE-3.
10 The novel DNA sequences of the present invention can be inserted into vectors which comprise nucleic acids encoding human ECE-3 or a functional equivalent. These vectors may be comprised of DNA or RNA; for most cloning purposes DNA vectors are preferred. Typical vectors include plasmids, modified viruses, bacteriophage, cosmids, yeast artificial chromosomes, and other forms of episomal or
15 integrated DNA that can encode a ECE-3 protein. It is well within the skilled artisan to determine an appropriate vector for a particular gene transfer or other use.

Included in the present invention are DNA sequences that hybridize to SEQ ID NO:1 under stringent conditions. By way of example, and not limitation, a procedure using conditions of high stringency is as follows: Prehybridization of filters
20 containing DNA is carried out for 2 hours to overnight at 65°C in buffer composed of 6X SSC, 5X Denhardt's solution, and 100 µg/ml denatured salmon sperm DNA. Filters are hybridized for 12 to 48 hrs at 65°C in prehybridization mixture containing 100 µg/ml denatured salmon sperm DNA and 5-20 X 10⁶ cpm of ³²P-labeled probe. Washing of filters is done at 37°C for 1 hr in a solution containing 2X SSC, 0.1%
25 SDS. This is followed by a wash in 0.1X SSC, 0.1% SDS at 50°C for 45 min. before autoradiography. Other procedures using conditions of high stringency would include either a hybridization step carried out in 5XSSC, 5X Denhardt's solution, 50% formamide at 42°C for 12 to 48 hours or a washing step carried out in 0.2X SSPE, 0.2% SDS at 65°C for 30 to 60 minutes.

30 Reagents mentioned in the foregoing procedures for carrying out high stringency hybridization are well known in the art. Details of the composition of these reagents can be found in, e.g., Sambrook et al., 1989, *Molecular Cloning: A Laboratory Manual*; Cold Spring Harbor Laboratory, Cold Spring Harbor, New York.

In addition to the foregoing, other conditions of high stringency which may be used are well known in the art.

The present invention also relates to a substantially purified form of the human ECE-3 protein, which comprises the amino acid sequence disclosed in Figure 2A-B and as set forth in SEQ ID NO:2.

The present invention also relates to biologically active fragments and/or mutants of the human ECE-3 protein comprising the amino acid sequence as set forth in SEQ ID NO:2, including but not necessarily limited to amino acid substitutions, deletions, additions, amino terminal truncations and carboxy-terminal truncations such that these mutations provide for proteins or protein fragments of diagnostic, therapeutic or prophylactic use and would be useful for screening for agonists and/or antagonists of ECE-3 function or other components of the endothelin signal pathway.

A preferred aspect of the present invention is disclosed in Figure 2A-B and is set forth as SEQ ID NO:2 in three letter code, and as herein set forth as follows:

Met Glu Pro Pro Tyr Ser Leu Thr Ala His Tyr Asp Glu Phe Gln Glu
Val Lys Tyr Val Ser Arg Cys Gly Ala Gly Gly Ala Arg Gly Ala Ser
Leu Pro Pro Gly Phe Pro Leu Gly Ala Ala Arg Ser Ala Thr Gly Ala
Arg Ser Gly Leu Pro Arg Trp Asn Arg Arg Glu Val Cys Leu Leu Ser
Gly Leu Val Phe Ala Ala Gly Leu Cys Ala Ile Leu Ala Ala Met Leu
Ala Leu Lys Tyr Leu Gly Pro Val Ala Ala Gly Gly Gly Ala Cys Pro
Glu Gly Cys Pro Glu Arg Lys Ala Phe Ala Arg Ala Ala Arg Phe Leu
Ala Ala Asn Leu Asp Ala Ser Ile Asp Pro Cys Gln Asp Phe Tyr Ser
Phe Ala Cys Gly Gly Trp Leu Arg Arg His Ala Ile Pro Asp Asp Lys
Leu Thr Tyr Gly Thr Ile Ala Ala Ile Gly Glu Gln Asn Glu Glu Arg
Leu Arg Arg Leu Leu Ala Arg Pro Gly Gly Gly Pro Gly Gly Ala Ala
Gln Arg Lys Val Arg Ala Phe Phe Arg Ser Cys Leu Asp Met Arg Glu
Ile Glu Arg Leu Gly Pro Arg Pro Met Leu Glu Val Ile Glu Asp Cys
Gly Gly Trp Asp Leu Gly Gly Ala Glu Glu Arg Pro Gly Val Ala Ala
Arg Trp Asp Leu Asn Arg Leu Leu Tyr Lys Ala Gln Gly Val Tyr Ser
Ala Ala Ala Leu Phe Ser Leu Thr Val Ser Leu Asp Asp Arg Asn Ser
Ser Arg Tyr Val Ile Arg Ile Asp Gln Asp Gly Leu Thr Leu Pro Glu
Arg Thr Leu Tyr Leu Ala Gln Asp Glu Asp Ser Glu Lys Ile Leu Ala
Ala Tyr Arg Val Phe Met Glu Arg Val Leu Ser Leu Leu Gly Ala Asp

Ala Val Glu Gln Lys Ala Gln Glu Ile Leu Gln Val Glu Gln Gln Leu
 Ala Asn Ile Thr Val Ser Glu Tyr Asp Asp Leu Arg Arg Asp Val Ser
 Ser Met Tyr Asn Lys Val Thr Leu Gly Gln Leu Gln Lys Ile Thr Pro
 His Leu Arg Trp Lys Trp Leu Leu Asp Gln Ile Phe Gln Glu Asp Phe
 5 Ser Glu Glu Glu Glu Val Val Leu Leu Ala Thr Asp Tyr Met Gln Gln
 Val Ser Gln Leu Ile Arg Ser Thr Pro His Arg Val Leu His Asn Tyr
 Leu Val Trp Arg Val Val Val Val Leu Ser Glu His Leu Ser Pro Pro
 Phe Arg Glu Ala Leu His Glu Leu Ala Gln Glu Met Glu Gly Ser Asp
 Lys Pro Gln Glu Leu Ala Arg Val Cys Leu Gly Gln Ala Asn Arg His
 10 Phe Gly Met Ala Leu Gly Ala Leu Phe Val His Glu His Phe Ser Ala
 Ala Ser Lys Ala Lys Val Gln Gln Leu Val Glu Asp Ile Lys Tyr Ile
 Leu Gly Gln Arg Leu Glu Glu Leu Asp Trp Met Asp Ala Glu Thr Arg
 Ala Ala Ala Arg Ala Lys Leu Gln Tyr Met Met Val Met Val Gly Tyr
 Pro Asp Phe Leu Leu Lys Pro Asp Ala Val Asp Lys Glu Tyr Glu Phe
 15 Glu Val His Glu Lys Thr Tyr Phe Lys Asn Ile Leu Asn Ser Ile Arg
 Phe Ser Ile Gln Leu Ser Val Lys Lys Ile Arg Gln Glu Val Asp Lys
 Ser Thr Trp Leu Leu Pro Pro Gln Ala Leu Asn Ala Tyr Tyr Leu Pro
 Asn Lys Asn Gln Met Val Phe Pro Ala Gly Ile Leu Gln Pro Thr Leu
 Tyr Asp Pro Asp Phe Pro Gln Ser Leu Asn Tyr Gly Gly Ile Gly Thr
 20 Ile Ile Gly His Glu Leu Thr His Gly Tyr Asp Asp Trp Gly Gly Gln
 Tyr Asp Arg Ser Gly Asn Leu Leu His Trp Trp Thr Glu Ala Ser Tyr
 Ser Arg Phe Leu Arg Lys Ala Glu Cys Ile Val Arg Leu Tyr Asp Asn
 Phe Thr Val Tyr Asn Gln Arg Val Asn Gly Lys His Thr Leu Gly Glu
 Asn Ile Ala Asp Met Gly Gly Leu Lys Leu Ala Tyr His Ala Tyr Gln
 25 Lys Trp Val Arg Glu His Gly Pro Glu His Pro Leu Pro Arg Leu Lys
 Tyr Thr His Asp Gln Leu Phe Phe Ile Ala Phe Ala Gln Asn Trp Cys
 Ile Lys Arg Arg Ser Gln Ser Ile Tyr Leu Gln Val Leu Thr Asp Lys
 His Ala Pro Glu His Tyr Arg Val Leu Gly Ser Val Ser Gln Phe Glu
 Glu Phe Gly Arg Ala Phe His Cys Pro Lys Asp Ser Pro Met Asn Pro
 30 Ala His Lys Cys Ser Val Trp (SEQ ID NO:2), which comprises the amino acid
 sequence of wild type human ECE-3 protein.

As with many enzymes, it is possible to modify many of the amino
 acids of ECE-3, particularly those which are not found within or in contact with the
 active site, and still retain substantially the same biological activity as the wild type

protein. Thus this invention includes modified ECE-3 polypeptides which have amino acid deletions, additions, or substitutions but that still retain substantially the same biological activity as ECE-3. It is generally accepted that single amino acid substitutions do not usually alter the biological activity of a protein (see, e.g.,

5 *Molecular Biology of the Gene*, Watson *et al.*, 1987, Fourth Ed., The Benjamin/Cummings Publishing Co., Inc., page 226; and Cunningham & Wells, 1989, *Science* 244:1081-1085). Accordingly, the present invention includes polypeptides where one amino acid substitution has been made in SEQ ID NO:2 wherein the polypeptides still retain substantially the same biological activity as ECE-3. The

10 present invention also includes polypeptides where two or more amino acid substitutions have been made in SEQ ID NO:2 wherein the polypeptides still retain substantially the same biological activity as ECE-3. In particular, the present invention includes embodiments where the above-described substitutions are conservative substitutions. In particular, the present invention includes embodiments

15 where the above-described substitutions do not occur within the active site of ECE-3.

One skilled in the art would also recognize that polypeptides that are functional equivalents of ECE-3 and have changes from the ECE-3 amino acid sequence that are small deletions or insertions of amino acids could also be produced by following the same guidelines, (i.e., minimizing the differences in amino acid

20 sequence between ECE-3 and related proteins. Small deletions or insertions are generally in the range of about 1 to 5 amino acids. The effect of such small deletions or insertions on the biological activity of the modified ECE-3 polypeptide can easily be assayed by producing the polypeptide synthetically or by making the required changes in DNA encoding ECE-3 and then expressing the DNA recombinantly and

25 assaying the protein produced by such recombinant expression.

The present invention also includes truncated forms of ECE-3 which contain the region comprising the active site of the enzyme. Such truncated proteins are useful in various assays described herein, for crystallization studies, and for structure-activity-relationship studies.

30 The present invention also relates to crude or substantially purified subcellular membrane fractions from the recombinant host cells (both prokaryotic and eukaryotic as well as both stably and transiently transformed cells) which contain the nucleic acid molecules of the present invention. These recombinant host cells express ECE-3 or a functional equivalent, which becomes post translationally associated with

an appropriate membrane (such as the cell membrane or the Golgi membrane) in a biologically active fashion. These subcellular membrane fractions will comprise either wild-type or mutant forms of human ECE-3 at levels substantially above endogenous levels and hence will be useful in various assays described throughout this specification. In other words, a specific use for such subcellular membranes involves expression of ECE-3 within the recombinant cell followed by isolation and substantial purification of the membranes away from other cellular components. These substantially purified membranes preparations, which again may be retrieved from a prokaryotic or eukaryotic host cell (including a human recombinant host cell line), will be especially useful in assays to determine the effect of a test substance on ECE-3 catalysis of a big ET precursor to the respective endothelin.

The present invention also relates to isolated nucleic acid molecules which are fusion constructions expressing fusion proteins useful in assays to identify compounds which modulate wild-type vertebrate ECE-3 activity, as well as generating antibodies against human ECE-3. A preferred aspect of this portion of the invention includes, but is not limited to, glutathione S-transferase (GST)-ECE-3 fusion constructs which include, but are not limited to, either the intracellular domain of human ECE-3 as an in-frame fusion at the carboxy terminus of the GST gene or the extracellular and transmembrane ligand binding domain of ECE-3 fused to an GST or immunoglobulin gene by methods known to one of ordinary skill in the art. Recombinant GST-ECE-3 fusion proteins may be expressed in various expression systems, including *Spodoptera frugiperda* (Sf21) insect cells (Invitrogen) using a baculovirus expression vector (pAcG2T, Pharmingen).

Any of a variety of procedures may be used to clone human ECE-3. These methods include, but are not limited to, (1) a RACE PCR cloning technique (Frohman, et al., 1988, *Proc. Natl. Acad. Sci. USA* 85: 8998-9002). 5' and/or 3' RACE may be performed to generate a full-length cDNA sequence. This strategy involves using gene-specific oligonucleotide primers for PCR amplification of human ECE-3 cDNA. These gene-specific primers are designed through identification of an expressed sequence tag (EST) nucleotide sequence which has been identified by searching any number of publicly available nucleic acid and protein databases; (2) direct functional expression of the human ECE-3 cDNA following the construction of a human ECE-3-containing cDNA library in an appropriate expression vector system; (3) screening a human ECE-3-containing cDNA library constructed in a bacteriophage

or plasmid shuttle vector with a labeled degenerate oligonucleotide probe designed from the amino acid sequence of the human ECE-3 protein; (4) screening a human ECE-3-containing cDNA library constructed in a bacteriophage or plasmid shuttle vector with a partial cDNA encoding the human ECE-3 protein. This partial cDNA is
5 obtained by the specific PCR amplification of human ECE-3 DNA fragments through the design of degenerate oligonucleotide primers from the amino acid sequence known for other kinases which are related to the human ECE-3 protein; (5) screening a human ECE-3-containing cDNA library constructed in a bacteriophage or plasmid shuttle vector with a partial cDNA or oligonucleotide with homology to a mammalian
10 ECE-3 protein. This strategy may also involve using gene-specific oligonucleotide primers for PCR amplification of human ECE-3 cDNA identified as an EST as described above; or (6) designing 5' and 3' gene specific oligonucleotides using SEQ ID NO: 1 as a template so that either the full-length cDNA may be generated by known RACE techniques, or a portion of the coding region may be generated by these
15 same known RACE techniques to generate and isolate a portion of the coding region to use as a probe to screen one of numerous types of cDNA and/or genomic libraries in order to isolate a full-length version of the nucleotide sequence encoding human ECE-3.

It is readily apparent to those skilled in the art that other types of
20 libraries, as well as libraries constructed from other cell types or species types, may be useful for isolating a human ECE-3-encoding DNA or a human ECE-3 homologue. Other types of libraries include, but are not limited to, cDNA libraries derived from other human cells.

It is readily apparent to those skilled in the art that suitable cDNA
25 libraries may be prepared from cells or cell lines which have ECE-3 activity. The selection of cells or cell lines for use in preparing a cDNA library to isolate a cDNA encoding human ECE-3 may be done by first measuring cell-associated ECE-3 activity using any known assay available for such a purpose.

Preparation of cDNA libraries can be performed by standard
30 techniques well known in the art. Well known cDNA library construction techniques can be found for example, in Sambrook et al., 1989, *Molecular Cloning: A Laboratory Manual*; Cold Spring Harbor Laboratory, Cold Spring Harbor, New York. Complementary DNA libraries may also be obtained from numerous commercial sources, including but not limited to Clontech Laboratories, Inc. and Stratagene.

It is also readily apparent to those skilled in the art that DNA encoding human ECE-3 may also be isolated from a suitable genomic DNA library. Construction of genomic DNA libraries can be performed by standard techniques well known in the art. Well known genomic DNA library construction techniques can be found in Sambrook, et al., *supra*. Genomic clones containing the ECE-3 gene can be obtained from commercially available human PAC or BAC libraries, e.g., from Research Genetics, Huntsville, AL. Alternatively, one may prepare genomic libraries, especially in P1 artificial chromosome vectors, from which genomic clones containing the ECE-3 can be isolated, using probes based upon the ECE-3 nucleotide sequences disclosed herein. Methods of preparing such libraries are known in the art (Ioannou et al., 1994, *Nature Genet.* 6:84-89).

In order to clone the human ECE-3 gene by one of the preferred methods, the amino acid sequence or DNA sequence of human ECE-3 or a homologous protein may be necessary. To accomplish this, the ECE-3 protein or a homologous protein may be purified and partial amino acid sequence determined by automated sequenators. It is not necessary to determine the entire amino acid sequence, but the linear sequence of two regions of 6 to 8 amino acids can be determined for the PCR amplification of a partial human ECE-3 DNA fragment. Once suitable amino acid sequences have been identified, the DNA sequences capable of encoding them are synthesized. Because the genetic code is degenerate, more than one codon may be used to encode a particular amino acid, and therefore, the amino acid sequence can be encoded by any of a set of similar DNA oligonucleotides. Only one member of the set will be identical to the human ECE-3 sequence but others in the set will be capable of hybridizing to human ECE-3 DNA even in the presence of DNA oligonucleotides with mismatches. The mismatched DNA oligonucleotides may still sufficiently hybridize to the human ECE-3 DNA to permit identification and isolation of human ECE-3 encoding DNA. Alternatively, the nucleotide sequence of a region of an expressed sequence may be identified by searching one or more available genomic databases. Gene-specific primers may be used to perform PCR amplification of a cDNA of interest from either a cDNA library or a population of cDNAs. As noted above, the appropriate nucleotide sequence for use in a PCR-based method may be obtained from SEQ ID NO: 1, either for the purpose of isolating overlapping 5' and 3' RACE products for generation of a full-length sequence coding for human ECE-3, or to isolate a portion of the nucleotide sequence coding for human

ECE-3 for use as a probe to screen one or more cDNA- or genomic-based libraries to isolate a full-length sequence encoding human ECE-3 or human ECE-3-like proteins.

This invention also includes vectors containing a ECE-3 gene, host cells containing the vectors, and methods of making substantially pure ECE-3 protein comprising the steps of introducing the ECE-3 gene into a host cell, and cultivating the host cell under appropriate conditions such that ECE-3 is produced. The ECE-3 so produced may be harvested from the host cells in conventional ways. Therefore, the present invention also relates to methods of expressing the human ECE-3 protein and biological equivalents disclosed herein, assays employing these gene products, recombinant host cells which comprise DNA constructs which express these proteins, and compounds identified through these assays which act as agonists or antagonists of ECE-3 activity.

The cloned human ECE-3 cDNA obtained through the methods described above may be recombinantly expressed by molecular cloning into an expression vector (such as pcDNA3.neo, pcDNA3.1, pCR2.1, pBlueBacHis2 or pLITMUS28) containing a suitable promoter and other appropriate transcription regulatory elements, and transferred into prokaryotic or eukaryotic host cells to produce recombinant human ECE-3. Techniques for such manipulations can be found described in Sambrook, et al., *supra*, are discussed at length in the Example section and are well known and easily available to the artisan of ordinary skill in the art. Therefore, another aspect of the present invention includes host cells that have been engineered to contain and/or express DNA sequences encoding the ECE-3. An expression vector containing DNA encoding a human ECE-3-like protein may be used for expression of human ECE-3 in a recombinant host cell. Such recombinant host cells can be cultured under suitable conditions to produce ECE-3 or a biologically equivalent form. Recombinant host cells may be prokaryotic or eukaryotic, including but not limited to, bacteria such as *E. coli*, fungal cells such as yeast, mammalian cells including, but not limited to, cell lines of human, bovine, porcine, monkey and rodent origin, and insect cells including but not limited to *Drosophila* and silkworm derived cell lines.

For instance, one insect expression system utilizes *Spodoptera frugiperda* (Sf21) insect cells (Invitrogen) in tandem with a baculovirus expression vector (pAcG2T, Pharmingen). Also, mammalian species which may be suitable and which are commercially available, include but are not limited to, L cells L-M(TK⁻)

(ATCC CCL 1.3), L cells L-M (ATCC CCL 1.2), Saos-2 (ATCC HTB-85), 293 (ATCC CRL 1573), Raji (ATCC CCL 86), CV-1 (ATCC CCL 70), COS-1 (ATCC CRL 1650), COS-7 (ATCC CRL 1651), CHO-K1 (ATCC CCL 61), 3T3 (ATCC CCL 92), NIH/3T3 (ATCC CRL 1658), HeLa (ATCC CCL 2), C1271 (ATCC CRL 1616),
5 BS-C-1 (ATCC CCL 26), MRC-5 (ATCC CCL 171) and CPAE (ATCC CCL 209).

The present invention is also directed to methods for screening for compounds which modulate the expression of DNA or RNA encoding a human ECE-3 protein. Compounds which modulate these activities may be DNA, RNA, peptides, proteins, or non-proteinaceous organic molecules. Compounds may modulate by
10 increasing or attenuating the expression of DNA or RNA encoding human ECE-3, or the function of human ECE-3. Compounds that modulate the expression of DNA or RNA encoding human ECE-3 or the biological function thereof may be detected by a variety of assays. The assay may be a simple "yes/no" assay to determine whether there is a change in expression or function. The assay may be made quantitative by
15 comparing the expression or function of a test sample with the levels of expression or function in a standard sample. Kits containing human ECE-3, antibodies to human ECE-3, or modified human ECE-3 may be prepared by known methods for such uses.

Chinese hamster ovary (CHO) cells are particularly suitable for expression of the ECE-3 protein because these cells express a large number of G-
20 proteins (including ETA and ETB) and contain a minimal amount of ECE activity (Xu et al., 1994, *Cell* 78: 473-485). Thus, it is likely that at least endothelin receptor ETA or ETB will be able to functionally couple the signal generated by interaction with an endothelin peptide generated by the catalytic activity of ECE-3, thus transmitting this signal to downstream effectors, eventually resulting in a measurable change in some
25 assayable component, e.g., cAMP level, expression of a reporter gene, hydrolysis of inositol lipids, or intracellular Ca^{2+} levels. It will also be within the purview of the skilled artisan to generate a CHO cell line which is stably or transiently transfected with a DNA molecule or DNA vector which expresses human ECE-3 and a DNA molecule or DNA vector which expresses an endothelin receptor, including but not
30 limited to a human ETA or human ETB receptor. It will also be within the purview of the skilled artisan to generate a CHO cell line which is stably or transiently transfected with a DNA molecule or DNA vector which expresses human ECE-3, a DNA molecule or DNA vector which expresses an endothelin receptor, including but not limited to a human ETA or human ETB receptor, and a DNA molecule or vector

which expresses either the endothelin prepropolypeptide or the respective big ET polypeptide. While there are numerous variations on this theme which will be evident to the artisan of ordinary skill, including different cell lines, different combinations of DNA molecules or DNA vectors from the endothelin pathway, as well as the stable or
5 transient transfection of the DNA molecule or vector of interest, the construction of the cell lines serves the purpose of conduction cell-based assay to test for modulators of ECE-3 activity or modulators of another step in the endothelin pathway. For example, a cell such as a CHO cell which is transformed with DNA molecules or DNA vectors which express human ECE-3 and a prepropolypeptide, respectively, will
10 be useful in assays to select compounds which modulate ECE-3 activity. These double-transformed or double-transfected cells are allowed to grow for a time sufficient to express human ECE-3 and the endothelin prepropolypeptide wherein the big ET substrate is generated. The transfected cells are harvested and resuspended in a sample assay buffer (plus test compound) and control assay buffer (minus test
15 compound) for an adequate period of time. The conditioned medium from the cells may be directly assayed by known enzyme immunoassay procedures for the presence of mature endothelin peptide. An antagonist of ECE-3 catalyzed conversion of big ET to mature endothelin will result in decreased concentration of processed endothelin versus the control while an agonist of ECE-3 catalyzed conversion to mature
20 endothelin will result in increased concentration of endothelin compared to control levels.

Therefore, the present invention relates to methods of expressing ECE-3 in recombinant systems and of identifying agonists and antagonists of ECE-3. The novel ECE-3 protein of the present invention is suitable for use in an assay procedure
25 for the identification of compounds which modulate the conversion of big ET to ET. Modulating ECE-3 activity, as described herein includes the inhibition or activation of the enzyme and also includes directly or indirectly affecting the normal regulation of the enzymatic activity of ECE-3. Compounds which modulate ECE-3 include agonists, antagonists and compounds which directly or indirectly affect regulation of
30 human ECE-3. When screening compounds in order to identify potential pharmaceuticals that specifically interact with a target protein, it is necessary to ensure that the compounds identified are as specific as possible for the target protein. To do this, it may necessary to screen the compounds against as wide an array as possible of proteins that are similar to the target receptor. Thus, in order to find compounds that

are potential pharmaceuticals that interact with ECE-3, it is necessary not only to ensure that the compounds interact with ECE-3 (the "plus target") and produce the desired pharmacological effect through ECE-3, it is also necessary to determine that the compounds do not interact with proteins B, C, D, etc. (the "minus targets"). In general, as part of a screening program, it is important to have as many minus targets as possible (see Hodgson, 1992, *Bio/Technology* 10:973-980, @ 980). Human ECE-3 proteins and the DNA molecules encoding this protein have the additional utility in that they can be used as "minus targets" in screens designed to identify compounds that specifically interact with other components of the endothelin pathway which effect signal transduction of ET-1, ET-2 and/or ET-3, including but not limited to ECE-1 and ECE-2.

A particular embodiment of the present invention includes a method for determining whether a substance is a potential agonist or antagonist of ECE-3 that comprises:

- (a) transfecting cells with an expression vector encoding ECE-3;
- (b) allowing the transfected cells to grow for a time sufficient to allow ECE-3 to be expressed;
- (c) harvesting the transfected cells and resuspending the cells in the presence of a known, labeled antagonist (including but not limited to phosphoramidon) or agonist of ECE-3 (i.e. ligand for ECE-3) in the presence and in the absence of the substance;
- (d) measuring the binding of the labeled ligand for ECE-3 where if the amount of binding of the known ligand is less in the presence of the substance than in the absence of the substance, then the substance is a potential agonist of ECE-3 activity. In a modification of the above-described method, step (c) is modified in that the cells are not harvested and resuspended but rather the radioactively labeled known ligand and the substance are contacted with the cells while the cells are attached to a substratum, e.g., tissue culture plates. The conditions under which step (c) of the method is practiced in this study and other disclosed within this specification are conditions that are typically used in the art for the study of protein-ligand interactions: e.g., physiological pH; salt conditions such as those represented by such commonly used buffers as PBS or in tissue culture media; a temperature of about 4°C to about 55°C. Such ligands need not necessarily be radiolabeled but can also be nonisotopic compounds that can be used to displace bound radiolabeled compounds or

that can be used as activators in functional assays. Compounds identified by the above method are likely to be agonists or antagonists of ECE-3 and may be peptides, proteins, or non-proteinaceous organic molecules.

5 The present invention also includes a method for determining whether a substance is capable of binding to ECE-3, i.e., whether the substance is a potential agonist or an antagonist of ECE-3, where the method comprises:

- (a) providing test cells by transfecting cells with an expression vector that directs the expression of ECE-3 in the cells;
- (b) exposing the test cells to the substance;
- 10 (c) measuring the amount of binding of the substance to ECE-3;
- (d) comparing the amount of binding of the substance to ECE-3 in the test cells with the amount of binding of the substance to control cells that have not been transfected with ECE-3;

wherein if the amount of binding of the substance is greater in the test
15 cells as compared to the control cells, the substance is capable of binding to ECE-3. Determining whether the substance is actually an agonist or antagonist can then be accomplished by the use of functional assays such as, e.g., the assay involving the ability of effect conversion of big ET to ET in the presence of ECE-3 and the substance of interest.

20 The conditions under which step (b) of the method is practiced are conditions that are typically used in the art for the study of protein-ligand interactions: e.g., physiological pH; salt conditions such as those represented by such commonly used buffers as PBS or in tissue culture media; a temperature of about 4°C to about 55°C.

25 A preferred method for determining whether a substance is capable of binding to endothelin converting enzyme-3 includes the following steps:

- (a) providing test cells by transfecting cells with an expression vector that directs the expression of endothelin converting enzyme-3 as set forth as SEQ ID NO:2 in the cells;
- 30 (b) exposing the test cells to the substance;
- (c) measuring the amount of binding of the substance to the endothelin converting enzyme-3;
- (d) comparing the amount of binding of the substance to the endothelin converting enzyme-3 in the test cells with the amount of binding of the

substance to control cells that have not been transfected with the expression vector that directs the expression of endothelin converting enzyme-3 as set forth as SEQ ID NO:2.

5 A preferred method for determining whether a substance is capable of modulating endothelin converting enzyme-3 activity includes the following steps:

- (a) providing test cells by transfecting cells with an expression vector that directs the expression of endothelin converting enzyme-3 as set forth as SEQ ID NO:2;
- (b) exposing the test cells to the substance;
- 10 (c) measuring the amount of an accumulated intracellular secondary message;
- (d) comparing the amount of the secondary message in the test cells in response to the substance with the amount of secondary message in test cells that have not been exposed to the substance.

15 An especially preferred method measures the amount of accumulated cAMP in a transfected or transformed host cell, such a CHO cell, that endogenously express ETA or ETB and contain minimal endogenous endothelial converting enzyme.

Another preferred screening method of the present invention includes a method for determining whether a substance is capable of modulating endothelin
20 converting enzyme-3 activity which involves some or all of the following steps:

- (a) providing test cells by transfecting cells with an expression vector that directs the expression of endothelin converting enzyme-3 as set forth as SEQ ID NO:2;
- (b) purifying membrane preparations comprising the endothelin
25 converting enzyme-3;
- (c) adding a test substance to the purified membrane preparations of step (b);
- (d) incubating the test substance-containing membrane preparation of step (c) with a substrate of endothelin converting enzyme-3;
- 30 (e) comparing the product generated from step (d) versus the amount of product generated from a membrane preparation containing the substrate of step (d) without addition of the test substance of step (c).

An especially preferred substrate for use in this enzyme assay is a substrate selected from the group consisting of big ET-1, big ET-2 and big ET-3.

The specificity of binding of compounds showing affinity for ECE-3 is shown by measuring the affinity of the compounds for recombinant cells expressing the protein or for membranes from these cells. Expression of the protein and screening for compounds that bind to ECE-3 or that inhibit the binding of a known, radiolabeled ligand of ECE-3 to these cells, or membranes prepared from these cells, provides an effective method for the rapid selection of compounds with high affinity for ECE-3. Such ligands need not necessarily be radiolabeled but can also be nonisotopic compounds that can be used to displace bound radiolabeled compounds or that can be used as activators in functional assays. Compounds identified by the above method are likely to be agonists or antagonists of ECE-3 and may be peptides, proteins, or non-proteinaceous organic molecules.

An embodiment of the present invention is determining various ligand binding affinities using a labeled ligand in the presence of varying concentration of unlabeled ligands. The activation of the second messenger pathway is determined by measuring the intracellular cAMP elicited by an agonist or antagonist at various concentration. Therefore, it is within the realm of screening for such compounds to use a transactivation assay wherein a host cell is transfected with a reporter construct wherein a reporter gene is fused downstream of a promoter and response element which is positively regulated by a secondary signal such as cAMP. For example, Chen et al. (1995, *Analytical Biochemistry* 226: 349-354) describe a colorimetric assay which utilizes a recombinant cell transfected with an expression vector encoding a G protein coupled receptor with a second expression vector containing a promoter with a cAMP responsive element fused to the LacZ gene. Activity of the overexpressed G-protein coupled receptor is measured as the expression and OD measurement of β -Gal. Therefore, another aspect of this portion of the invention includes a non-radioactive method for determining whether a substance is a potential agonist or antagonist of ECE-3 that comprises:

(a) stably transfecting or transforming cells with an expression vector encoding ECE-3, wherein these recombinant host cells express biologically active amounts of a G-protein coupled receptor which transmits a biological signal in response to binding with an endothelin;

(b) transiently or stably transfecting the recombinant host cell line of step (a) with an expression vector which comprises a cAMP-inducible promoter fused to a colorimetric gene such as LacZ;

(b) allowing the transfected cells to grow for a time sufficient to allow ECE-3 to be expressed;

(c) harvesting the transfected cells and resuspending the cells in the presence of a known agonist of ECE-3 and/or in both the presence and absence of the test compound;

(d) measuring the binding of the known agonist and test compound to expressed ECE-3 by a colorimetric assay which measures expression off the cAMP-inducible promoter and comparing expression levels in the presence of the known agonist as well as in the presence and absence of the unknown substance so as to determine whether the unknown substance acts as either a potential agonist or antagonist of ECE-3.

It is also possible to transfect or transform the above cells with a construct comprising a third gene wherein this third gene encodes G-protein coupled receptor which interacts with endothelins, such as ETA or ETB. The assays described above can be carried out with cells that have been transiently or stably transfected or stably transformed with expression vectors which encode ECE-3. Transfection is meant to include any method known in the art for introducing ECE-3 into the test cells. For example, transfection includes calcium phosphate or calcium chloride mediated transfection, lipofection, infection with a retroviral construct containing ECE-3, and electroporation. Transformation is meant to encompass a genetic change to the target cell resulting from an incorporation of DNA.

The DNA molecules, RNA molecules, recombinant protein and antibodies of the present invention may be used to screen and measure levels of human ECE-3. The recombinant proteins, DNA molecules, RNA molecules and antibodies lend themselves to the formulation of kits suitable for the detection and typing of human ECE-3. Such a kit would comprise a compartmentalized carrier suitable to hold in close confinement at least one container. The carrier would further comprise reagents such as recombinant ECE-3 or anti-ECE-3 antibodies suitable for detecting human ECE-3. The carrier may also contain a means for detection such as labeled antigen or enzyme substrates or the like.

A variety of mammalian expression vectors may be used to express recombinant human ECE-3 in mammalian cells. Expression vectors are defined herein as DNA sequences that are required for the transcription of cloned DNA and the translation of their mRNAs in an appropriate host. Such vectors can be used to

express eukaryotic DNA in a variety of hosts such as bacteria, blue green algae, plant cells, insect cells and animal cells. Specifically designed vectors allow the shuttling of DNA between hosts such as bacteria-yeast or bacteria-animal cells. An appropriately constructed expression vector should contain: an origin of replication
5 for autonomous replication in host cells, selectable markers, a limited number of useful restriction enzyme sites, a potential for high copy number, and active promoters. A promoter is defined as a DNA sequence that directs RNA polymerase to bind to DNA and initiate RNA synthesis. A strong promoter is one which causes mRNAs to be initiated at high frequency.

10 Expression vectors may include, but are not limited to, cloning vectors, modified cloning vectors, specifically designed plasmids or viruses. Commercially available mammalian expression vectors which may be suitable for recombinant human ECE-3 expression, include but are not limited to, pcDNA3.neo (Invitrogen), pcDNA3.1 (Invitrogen), pCI-neo (Promega), pLITMUS28, pLITMUS29,
15 pLITMUS38 and pLITMUS39 (New England Biolabs), pcDNA1, pcDNA1amp (Invitrogen), pcDNA3 (Invitrogen), pMC1neo (Stratagene), pXT1 (Stratagene), pSG5 (Stratagene), EBO-pSV2-neo (ATCC 37593) pBPV-1(8-2) (ATCC 37110), pdBPV-MMTneo(342-12) (ATCC 37224), pRSVgpt (ATCC 37199), pRSVneo (ATCC 37198), pSV2-dhfr (ATCC 37146), pUCTag (ATCC 37460), and IZD35 (ATCC
20 37565).

Also, a variety of bacterial expression vectors may be used to express recombinant human ECE-3 in bacterial cells. Commercially available bacterial expression vectors which may be suitable for recombinant human ECE-3 expression include, but are not limited to pCR2.1 (Invitrogen), pET11a (Novagen), lambda gt11
25 (Invitrogen), and pKK223-3 (Pharmacia).

In addition, a variety of fungal cell expression vectors may be used to express recombinant human ECE-3 in fungal cells. Commercially available fungal cell expression vectors which may be suitable for recombinant human ECE-3 expression include but are not limited to pYES2 (Invitrogen) and *Pichia* expression
30 vector (Invitrogen).

Also, a variety of insect cell expression vectors may be used to express recombinant protein in insect cells. Commercially available insect cell expression vectors which may be suitable for recombinant expression of human ECE-3 include

but are not limited to pBlueBacIII and pBlueBacHis2 (Invitrogen). and pAcG2T (Pharmingen).

5 The assays described above can be carried out with cells that have been transiently or stably transfected with ECE-3. The expression vector may be introduced into host cells via any one of a number of techniques including but not limited to transformation, transfection, protoplast fusion, and electroporation. Transfection is meant to include any method known in the art for introducing ECE-3 into the test cells. For example, transfection includes calcium phosphate or calcium chloride mediated transfection, lipofection, infection with a retroviral construct containing ECE-3, and electroporation. The expression vector-containing cells are individually analyzed to determine whether they produce human ECE-3 protein. Identification of human ECE-3 expressing cells may be done by several means, including but not limited to immunological reactivity with anti-human ECE-3 antibodies, labeled ligand binding, the presence of host cell-associated human ECE-3 activity via the conversion of big ET to ET.

15 Expression of human ECE-3 DNA may also be performed using *in vitro* produced synthetic mRNA. Synthetic mRNA can be efficiently translated in various cell-free systems, including but not limited to wheat germ extracts and reticulocyte extracts, as well as efficiently translated in cell based systems, including but not limited to microinjection into frog oocytes, with microinjection into frog oocytes being preferred.

To determine the human ECE-3 cDNA sequence(s) that yields optimal levels of human ECE-3, cDNA molecules including but not limited to the following can be constructed: a cDNA fragment containing the full-length open reading frame for human ECE-3 as well as various constructs containing portions of the cDNA encoding only specific domains of the protein or rearranged domains of the protein. All constructs can be designed to contain none, all or portions of the 5' and/or 3' untranslated region of a human ECE-3 cDNA. The expression levels and activity of human ECE-3 can be determined following the introduction, both singly and in combination, of these constructs into appropriate host cells. Following determination of the human ECE-3 cDNA cassette yielding optimal expression in transient assays, this ECE-3 cDNA construct is transferred to a variety of expression vectors (including recombinant viruses), including but not limited to those for mammalian cells, plant cells, insect cells, oocytes, bacteria, and yeast cells.

Following expression of human ECE-3 in a host cell, ECE-3 protein may be recovered to provide ECE-3 protein in active form. Several ECE-3 protein purification procedures are available and suitable for use. Recombinant ECE-3 protein may be purified from cell lysates and extracts by various combinations of, or
5 individual application of salt fractionation, ion exchange chromatography, size exclusion chromatography, hydroxylapatite adsorption chromatography and hydrophobic interaction chromatography. In addition, recombinant ECE-3 protein can be separated from other cellular proteins by use of an immunoaffinity column made with monoclonal or polyclonal antibodies specific for full-length ECE-3 protein, or
10 polypeptide fragments of ECE-3 protein.

Polyclonal or monoclonal antibodies may be raised against human ECE-3 or a synthetic peptide (usually from about 9 to about 25 amino acids in length) from a portion of human ECE-3 as disclosed in SEQ ID NO:2. Monospecific antibodies to human ECE-3 are purified from mammalian antisera containing
15 antibodies reactive against human ECE-3 or are prepared as monoclonal antibodies reactive with human ECE-3 using the technique of Kohler and Milstein (1975, *Nature* 256: 495-497). Monospecific antibody as used herein is defined as a single antibody species or multiple antibody species with homogenous binding characteristics for human ECE-3. Homogenous binding as used herein refers to the ability of the
20 antibody species to bind to a specific antigen or epitope, such as those associated with human ECE-3, as described above. Human ECE-3-specific antibodies are raised by immunizing animals such as mice, rats, guinea pigs, rabbits, goats, horses and the like, with an appropriate concentration of human ECE-3 protein or a synthetic peptide generated from a portion of human ECE-3 with or without an immune adjuvant.

25 Preimmune serum is collected prior to the first immunization. Each animal receives between about 0.1 mg and about 1000 mg of human ECE-3 protein associated with an acceptable immune adjuvant. Such acceptable adjuvants include, but are not limited to, Freund's complete, Freund's incomplete, alum-precipitate, water in oil emulsion containing *Corynebacterium parvum* and tRNA. The initial
30 immunization consists of human ECE-3 protein or peptide fragment thereof in, preferably, Freund's complete adjuvant at multiple sites either subcutaneously (SC), intraperitoneally (IP) or both. Each animal is bled at regular intervals, preferably weekly, to determine antibody titer. The animals may or may not receive booster injections following the initial immunization. Those animals receiving booster

injections are generally given an equal amount of human ECE-3 in Freund's incomplete adjuvant by the same route. Booster injections are given at about three week intervals until maximal titers are obtained. At about 7 days after each booster immunization or about weekly after a single immunization, the animals are bled, the
5 serum collected, and aliquots are stored at about -20°C.

Monoclonal antibodies (mAb) reactive with human ECE-3 are prepared by immunizing inbred mice, preferably Balb/c, with human ECE-3 protein. The mice are immunized by the IP or SC route with about 1 mg to about 100 mg, preferably about 10 mg, of human ECE-3 protein in about 0.5 ml buffer or saline
10 incorporated in an equal volume of an acceptable adjuvant, as discussed above. Freund's complete adjuvant is preferred. The mice receive an initial immunization on day 0 and are rested for about 3 to about 30 weeks. Immunized mice are given one or more booster immunizations of about 1 to about 100 mg of human ECE-3 in a buffer solution such as phosphate buffered saline by the intravenous (IV) route.

15 Lymphocytes, from antibody positive mice, preferably splenic lymphocytes, are obtained by removing spleens from immunized mice by standard procedures known in the art. Hybridoma cells are produced by mixing the splenic lymphocytes with an appropriate fusion partner, preferably myeloma cells, under conditions which will allow the formation of stable hybridomas. Fusion partners may include, but are not
20 limited to: mouse myelomas P3/NS1/Ag 4-1; MPC-11; S-194 and Sp 2/0, with Sp 2/0 being preferred. The antibody producing cells and myeloma cells are fused in polyethylene glycol, about 1000 mol. wt., at concentrations from about 30% to about 50%. Fused hybridoma cells are selected by growth in hypoxanthine, thymidine and aminopterin supplemented Dulbecco's Modified Eagles Medium (DMEM) by
25 procedures known in the art. Supernatant fluids are collected from growth positive wells on about days 14, 18, and 21 and are screened for antibody production by an immunoassay such as solid phase immunoradioassay (SPIRA) using human ECE-3 as the antigen. The culture fluids are also tested in the Ouchterlony precipitation assay to determine the isotype of the mAb. Hybridoma cells from antibody positive wells
30 are cloned by a technique such as the soft agar technique of MacPherson, 1973, *Soft Agar Techniques*, in *Tissue Culture Methods and Applications*, Kruse and Paterson, Eds., Academic Press.

Monoclonal antibodies are produced *in vivo* by injection of pristine primed Balb/c mice, approximately 0.5 ml per mouse, with about 2×10^6 to about $6 \times$

10⁶ hybridoma cells about 4 days after priming. Ascites fluid is collected at approximately 8-12 days after cell transfer and the monoclonal antibodies are purified by techniques known in the art.

In vitro production of anti-human ECE-3 mAb is carried out by
5 growing the hybridoma in DMEM containing about 2% fetal calf serum to obtain sufficient quantities of the specific mAb. The mAb are purified by techniques known in the art.

Antibody titers of ascites or hybridoma culture fluids are determined by various serological or immunological assays which include, but are not limited to,
10 precipitation, passive agglutination, enzyme-linked immunosorbent antibody (ELISA) technique and radioimmunoassay (RIA) techniques. Similar assays are used to detect the presence of human ECE-3 in body fluids or tissue and cell extracts.

It is readily apparent to those skilled in the art that the above described methods for producing monospecific antibodies may be utilized to produce antibodies
15 specific for human ECE-3 peptide fragments, or full-length human ECE-3.

Human ECE-3 antibody affinity columns are made, for example, by adding the antibodies to Affigel-10 (Biorad), a gel support which is pre-activated with N-hydroxysuccinimide esters such that the antibodies form covalent linkages with the
20 agarose gel bead support. The antibodies are then coupled to the gel via amide bonds with the spacer arm. The remaining activated esters are then quenched with 1M ethanolamine HCl (pH 8). The column is washed with water followed by 0.23 M glycine HCl (pH 2.6) to remove any non-conjugated antibody or extraneous protein. The column is then equilibrated in phosphate buffered saline (pH 7.3) and the cell
25 culture supernatants or cell extracts containing full-length human ECE-3 or human ECE-3 protein fragments are slowly passed through the column. The column is then washed with phosphate buffered saline until the optical density (A₂₈₀) falls to background, then the protein is eluted with 0.23 M glycine-HCl (pH 2.6). The purified human ECE-3 protein is then dialyzed against phosphate buffered saline.

Pharmaceutically useful compositions comprising modulators of
30 human ECE-3 may be formulated according to known methods such as by the admixture of a pharmaceutically acceptable carrier. Examples of such carriers and methods of formulation may be found in Remington's Pharmaceutical Sciences. To form a pharmaceutically acceptable composition suitable for effective administration, such compositions will contain an effective amount of the protein, DNA, RNA,

modified human ECE-3, or either ECE-3 agonists or antagonists including tyrosine kinase activators or inhibitors.

Therapeutic or diagnostic compositions of the invention are administered to an individual in amounts sufficient to treat or diagnose disorders. The effective amount may vary according to a variety of factors such as the individual's condition, weight, sex and age. Other factors include the mode of administration.

The pharmaceutical compositions may be provided to the individual by a variety of routes such as subcutaneous, topical, oral and intramuscular.

The term "chemical derivative" describes a molecule that contains additional chemical moieties which are not normally a part of the base molecule. Such moieties may improve the solubility, half-life, absorption, etc. of the base molecule. Alternatively the moieties may attenuate undesirable side effects of the base molecule or decrease the toxicity of the base molecule. Examples of such moieties are described in a variety of texts, such as Remington's Pharmaceutical Sciences.

Compounds identified according to the methods disclosed herein may be used alone at appropriate dosages. Alternatively, co-administration or sequential administration of other agents may be desirable.

The present invention also has the objective of providing suitable topical, oral, systemic and parenteral pharmaceutical formulations for use in the novel methods of treatment of the present invention. The compositions containing compounds identified according to this invention as the active ingredient can be administered in a wide variety of therapeutic dosage forms in conventional vehicles for administration. For example, the compounds can be administered in such oral dosage forms as tablets, capsules (each including timed release and sustained release formulations), pills, powders, granules, elixirs, tinctures, solutions, suspensions, syrups and emulsions, or by injection. Likewise, they may also be administered in intravenous (both bolus and infusion), intraperitoneal, subcutaneous, topical with or without occlusion, or intramuscular form, all using forms well known to those of ordinary skill in the pharmaceutical arts.

Advantageously, compounds of the present invention may be administered in a single daily dose, or the total daily dosage may be administered in divided doses of two, three or four times daily. Furthermore, compounds for the present invention can be administered in intranasal form via topical use of suitable

intranasal vehicles, or via transdermal routes, using those forms of transdermal skin patches well known to those of ordinary skill in that art. To be administered in the form of a transdermal delivery system, the dosage administration will, of course, be continuous rather than intermittent throughout the dosage regimen.

5 For combination treatment with more than one active agent, where the active agents are in separate dosage formulations, the active agents can be administered concurrently, or they each can be administered at separately staggered times.

10 The dosage regimen utilizing the compounds of the present invention is selected in accordance with a variety of factors including type, species, age, weight, sex and medical condition of the patient; the severity of the condition to be treated; the route of administration; the renal, hepatic and cardiovascular function of the patient; and the particular compound thereof employed. A physician or veterinarian of ordinary skill can readily determine and prescribe the effective amount of the drug
15 required to prevent, counter or arrest the progress of the condition. Optimal precision in achieving concentrations of drug within the range that yields efficacy without toxicity requires a regimen based on the kinetics of the drug's availability to target sites. This involves a consideration of the distribution, equilibrium, and elimination of a drug.

20 The following examples are provided to illustrate the present invention without, however, limiting the same hereto.

EXAMPLE 1

Isolation and Characterization of DNA Molecules Encoding Human ECE-3

25 There are two previously isolated ECE's, ECE-1 and ECE-2. The EST hsubn_1f12.x00 was found in a GSC database query using a number of full length human zinc metalloprotease protein sequences. A blastn search of the Merck.EST database queried with hsubn_1f12.x00 picked up only one other mouse EST
30 AA387792. A blastn against all of GenBank (Merck.DNA) hit bovine ECE-2 (U27341) with about 90% similarity. A Blastx query against Merck.PROTEIN resulted in finding 85% similarity to human ECE-1 (D43698) unigene class Hs.88611. The full length cDNA to hsubn_1f12.x00 was cloned and sequenced and this 1497 base pair cDNA was reblasted. Blastn against Merck.DNA again hit the bovine ECE-

2 (U27341) complete mRNA sequence with 90% identity. The second highest hit was to an EST entered 10 April 1998 to a human mRNA from KIAA0604 (ab011176) at 89% similarity. Blastx also hit the KIAA0604 sequence in the protein form. This human KIAA0604 protein sequence is 89% similar to the bovine ECE-1 sequence and 74% similar to human ECE-1. This indicates that KIAA0604 is most likely an ortholog of bovine ECE-2 and a paralog of human ECE-1. Human ECE-1 protein is also 89% similar to bovine ECE-2. Since the mouse hsubn_1f12.x00 sequence is 89% similar to both bovine ECE-2 and to human KIAA0604, it probably represent the mouse ortholog of the ECE-2 gene.

In a further search of the public database, an EST corresponding to a third member of this family was found, and a full-length sequence was isolated by EST sequencing and RACE (Rapid Amplification of cDNA Ends). A unigene search looking for endothelin converting enzyme hit index class Hs.26880 which consists of 3 ESTs and is annotated as being 44% similar to the rat ECE-1. The three ESTs represent 2 Image clones, which have the following designation and nucleotide sequence:

1. AA523527:

EST Id: 1168146; EST name: ni45g12.s1;

GenBank Acc.#: AA523527; GenBank gi: 2264239;

Clone Id: IMAGE:979846 (3') from NCI;

CTTTGCAGCA AGAACACAGC GAAGGTGGGG CCCGTACAAT CCAGCCTGGC AGAGGGTCTG
 GCCCCCTTAG AGCAGAATCT GGGGACCCCA GTATATTTCC CTCACAGCCC CCCAAAGTCC
 AGCCTCACCC TGCTCCAGGC CCCTCCTGAA GTGAGGGGCA GCAGGGGGAC CGGGTCCTGG
 AGGGGCTGGA AGGCAGGTGG TGCCCAGAGC GGGGCTGGCA CCGGGTGCAT GCCTGCCCCG
 GTAGCCAGCA GGAGGTGATT CGTGCGGGGG CAGTGGGGGC GTGCAGGCGG GCAGCAAGGC
 TCACCACACG GAACACTTGT GGGCAGGGTT CATGGGTGAG TCCTTGGGAC AGTGGAAGGC
 CCGGCCAAAC TCCTCAAAC TNGACACACT GCCCAGCACC CTGTAGTGCT CAGGGGCATG
 CTTGTCAGTC AGCAACTGCA GGTAGATGGA CTGCGACCGC GCTTGATGCA CAGTTTTGGG
 AAAAGGCATT AAAAG (SEQ ID NO:3);

2. R61440:

EST Id: 238195; EST name: yh15h02.r1;

GenBank Acc.#: R61440; GenBank gi: 832135;

GDB Id: 410527;

Clone Id: 37986 (5);

GGTCGGCTAC CCGGACTTCC TGCTGAAACC CGATGCTGTG GACAAGGAGT ATGAGTTTGA
 GGTCCATGAG AAGACCTACT TCAAGAACAT CTTGAACAGC ATCCGCTTCA GCATCCAGCT
 5 CTCAGTTAAG AAGATTTCGGC AGGAGGTGGA CAAGTCCACG TGGCTGCTCC CCCCACAGGC
 GCTCAATGCC TACTATCTAC CCAACAAGAA CCAGATGGTG TTCCCCGCGG GCATCCTGCA
 GCCCACCCTG TACGACCCTG ACTTCCCACA GTCTCTCAAC TACGGGGGCA TCGGCACCAT
 CATTGGACAT GAGCTGACCC ACGGCTACGA CGGACTGGGG GGGCCAGTAT GACCGCTCAG
 GGAACCTGCT TGCCTGGTG GGACGGAGGC TTCCTTACAG CCGNTTTCCT GCGAAAGGCT
 10 GAGTGCATCG TTCCCTNTTT TATGGACAAC TTTCAATGTN TTACAACCAG GCGGTGAACG
 GGAAACACAN GTTTGGGAGA ACATCGCAGT ATGGGGCGGN CTTAAGTTGG CTTACCACGC
 TATTAGAGTT GGTTCGGA NGCCCCAGG AGCACCATT CCCGGTTAAA TACANACTGA
 ACCAGT (SEQ ID NO:4); and,

15 3. R61395:
 EST Id: 238150; EST name: yh15h02.s1;
 GenBank Acc. #: R61395; GenBank gi: 832090;
 GDB Id: 410527
 Clone Id: 37986 (3)

20 TTTTTTTTTT TAACAGTGCA GTGATTATT GACCAGACTT TGCAGCAAGA ACACAGCGAA
 GGTGGGGCCC GTACAATCCA GCCTGGCAGA GGGTCTGGCC CCCTTAGAGC AGAATCTGGG
 GACCCCAGTA TATTTCCCTC ACAGCCCCC AAAGTCCAGC CTCACCCTGC TCCAGGCCCC
 TCCTGAAGTG AGGGGCAGCA GGGGGACCGG AGTCCTGGAG GGGCTGGAAG GCAGGTGGTG
 25 CCCAGAGCGG GGCTGGCACC GGGTGCATGC CTGCCCCGGT AGCCAGCAGG AGGTNATTCG
 TNCGGGGGCA GTNGGGGCNT GCAGGCGGGC ANCAGGNTTC ACCACACGGA AC
 (SEQ ID NO:5).

30 R61440 is a 5' EST 606 bp long which hits KIAA0604 with 60% similarity over only
 a portion of the full length EST (167/276 bp). No similar ESTs were found during
 this search of the public database. The two 3' sequences are identical to each other
 and to no other EST. The above ESTs may also be viewed at the National Center for
 Biotechnology Information (NCBI) homepage.

The full-length ECE-3 cDNA sequence was obtained by 5' RACE-PCR. First, the IMAGE clone 37986, from which the ESTs yh15h02.r1 (GenBank Acc. #: R61440) and yh15h02.s1 (GenBank Acc. #: R61395) were derived, and the IMAGE clone 979846 (GenBank Acc. #: AA523527) were obtained from Research Genetics and resequenced to correct errors in the EST sequences. This sequence was compared with those of the other ECE family members (ECE-1 and ECE-2) in the public databases, and it was determined that the 3' terminus of the gene was present in the IMAGE clone 37986 and IMAGE clone 979846 sequence. The 5' sequence was incomplete, however, and was obtained by 5' RACE. Two rounds of 5' RACE PCR were required to obtain the full length ECE-3 sequence; in both cases nested PCR reactions were carried out. The first round of PCR utilized gene specific primers 1-4 below (SEQ ID NO:6-9), based on the sequence of IMAGE clones 979846 and 37986 (979846 provided 244bp of 5' sequence that was not present in the public databases), using the Advantage cDNA PCR Kit (Clontech#K1905-1), and human fetal brain Marathon-Ready cDNA (Clontech #7402-1). Adaptor primers AP-1 and AP-2 were supplied by the manufacturer (Clontech). The first round RACE-PCR products were sequenced and gave 930 bp of additional ECE-3 sequence. Based on this sequence, further gene specific RACE-PCR primers (5-7 below, SEQ ID NO:10-12) were synthesized and used to amplify further 5' sequence, using the human ovary Marathon-Ready cDNA (Clontech #7417-1), and the Advantage-GC cDNA PCR Kit (Clontech #K1907-1). This produced a cDNA of 2894 nucleotides (see SEQ ID NO:1), which corresponded to the size of the band on the northern blot (see Example 2), and had a clear Kozak consensus start site (GGCGCCATGG, nucleotides 206-215 of SEQ ID NO:1), indicating that this sequence does indeed represent the full length ECE-3 gene.

25

1. 5'-GAAGTCAGGGTCGTACAGGGTG-3' (SEQ ID NO:6)
2. 5'-CTTGTTGGGTAGATAGTAGGC-3' (SEQ ID NO:7)
3. 5'-CTGGATGCTGAAGCGGATGCTGTTC-3' (SEQ ID NO:8)
4. 5'-CCTCAAACATCATACTCCTTGTCCAC-3' (SEQ ID NO:9)
- 30 5. 5'-CCTTGTTGTACATGGAGCTGACATC-3' (SEQ ID NO:10)
6. 5'-CCTTCTGTTCCACAGCGTCTGCAC-3' (SEQ ID NO:11)
7. 5'-GGTGAGCCCATCCTGGTCAATGCG-3' (SEQ ID NO:12).

PCR conditions were as follows: 94°C for 1min, 5 cycles of 94°C 10 sec, 72°C 4 min; 5 cycles of 94°C 10 sec, 70°C 4 min; 20 cycles for 94°C 10 sec, 68°C 4 min and 68°C for 10 min. PCR products were then cloned using the Zero Blunt PCR Cloning Kit (Invitrogen #K2700-20) and sequenced.

5 Once the full-length human ECE-3 cDNA sequence was obtained, a full-length human ECE-3 cDNA clone was then produced by PCR from both human fetal brain Marathon-Ready cDNA (Clontech #7402-1) and human ovary Marathon-Ready cDNA (Clontech #7417-1). Sequencing of each product gave the same sequence, showing that the ECE-3 mRNA is the same in both tissues. Two pairs of primers
10 were used:

1. forward: 5'-GCTCGGCTGCGCTGCGGCTCAG-3' (SEQ ID NO:13)
 reverse: 5'-GGTCCTGGAGGGGCTGGAAGG-3' (SEQ ID NO:14)
2. forward: 5'-CATCCCGTAGCCCAGGTGGC-3' (SEQ ID NO:15)
 reverse: 5'-GCCAGCAGGAGGTGATTCGTGCG-3' (SEQ ID NO:16)

15 PCR conditions were as follows: 94°C for 1 min, 32 cycles for 94°C 12 sec and 68°C 4 min, then 68°C for 10 min. This primary PCR amplification was subjected to nested PCR with primer pair 2 (SEQ ID NOs: 15 and 16). PCR products were subcloned and confirmed by DNA sequencing.

 Radiation hybrid mapping was done with the GeneBridge4 panel (Gyapay et
20 al., 1996) consisting of 93 radiation hybrid clones (Research Genetics). Primers had sequences:
 forward: 5'-GTCCCCCTGCTGCCCCCTCACTTCAG-3' (SEQ ID NO:17); and
 reverse: 5'-CCAGACTTTGCAGCAAGAACACAGC-3' (SEQ ID NO:18), and
 produced the expected band of 175 bp. AmpliTaq Gold (Perkin Elmer) was
25 performed with cycling parameters: 94°C for 1 min; 94°C for 20 sec, 70°C for 2 min, 32 cycles; 70°C for 5 min. Results were submitted to the Whitehead Institute Genome Center server, <http://www-genome.wi.mit.edu/cgi-bin/contig/rhmapper.pl>, and gave similar results. ECE-3 mapped to chromosome 2q, between markers
 CHLC.GATA12H10.14 and D2S331, 10.65 cR from CHLC.GATA12H10.14
30 (lod>15).

 Therefore, the exemplified cDNA molecule is 2894 base pairs, with an open reading frame of 2325 base pairs, corresponding to a protein of 775 amino acids. Radiation hybrid mapping assigns this gene to chromosome 2q37, in a region that has not been linked to any human disease that might logically be due to ECE mutation.

EXAMPLE 2

5 Northern Analysis of Human ECE-3 Expression

Four blots were used for Northern analysis: Human Brain Multiple Tissue Northern (MTN) Blot II (#7755-1); Human Brain Multiple Tissue Northern (MTN) Blot III (#7750-1); Human Multiple Tissue Northern (MTN) Blot (#7760-1); Human Multiple Tissue Northern (MTN) Blot II (#7759-1). A DNA hybridization probe was
10 generated from cDNA sources as disclosed in Example 1 using the following primers:
Forward: 5' CTCCTGCTGAAACCCGATGC 3' (SEQ ID NO:19);
Reverse: 5' CCAGACTTTGCAGCAAGAACACAGC 3' (SEQ ID NO:20)

The DNA sequence of the probe is as follows:

CTTCCTGCTGAAACCCGATGCTGTGGACAAGGAGTATGAGTTTGAGGTCCATGAGAAGACCTACTTCAA
15 GAACATCTTGAACAGCATCCGCTTCAGCATCCAGCTCTCAGTTAAGAAGATTCGGCAGGAGGTGGACAA
GTCCACGTGGCTGCTCCCCCACAGGCGCTCAATGCCTACTATCTACCCAACAAGAACCAGATGGTGT
CCCCGCGGGCATCCTGCAGCCACCCTGTACGACCCTGACTTCCCACAGTCTCTCAACTACGGGGGCAT
CGGCACCATCATTGGACATGAGCTGACCCACGGCTACGACGACTGGGGGGGCCAGTATGACCGCTCAGG
GAACCTGCTGCACTGGTGGACGGAGGCCTCTACAGCCGCTTCCTGCGAAAGGCTGAGTGCATCGTCCG
20 TCTCTATGACAACTTCACTGTCTACAACCAGCGGGTGAACGGGAAACACACGCTTGGGGAGAACATCGC
AGATATGGGCGGCCTCAAGCTGGCCTACCACGCCTATCAGAAGTGGGTGCGGGAGCACGGCCCAGAGCA
CCCACTTCCCCGGCTCAAGTACACACATGACCAGCTCTTCTTCATTGCCTTTGCCCAGAACTGGTGCAT
CAAGCGGCGGTGCGAGTCCATCTACCTGCAGGTGCTGACTGACAAGCATGCCCCCTGAGCACTACAGGGT
GCTGGGCAGTGTGTCCAGTTTGAGGAGTTTGCCCGGGCTTTCCACTGTCCCAAGGACTCACCCATGAA
25 CCCTGCCCACAAGTGTTCGTGTGGTGAGCCTGGCTGCCCCGCTGCACGCCCCCACTGCCCCCGCACGA
ATCACCTCCTGCTGGCTACCGGGGCAGGCATGCACCCGGTGCCAGCCCCGCTCTGGGCACCACCTGCCT
TCCAGCCCCCTCCAGGACCCGGTCCCCCTGCTGCCCCCTCACTTCAGGAGGGGCCTGGAGCAGGGTGAGGC
TGGACTTTGGGGGGCTGTGAGGGAAATATACTGGGGTCCCCAGATTCTGCTCTAAGGGGGCCAGACCCT
CTGCCAGGCTGGATTGTACGGGGCCCCACCTTCGCTGTGTTCTTGCTGCAAAGTCTGG
30 (SEQ ID NO:21).

Twenty five to fifty nanograms of probe was labeled with 5 ul of [α - 32 P] dCTP (3000Ci/mmol, 10mCi/ml) with a DECAprime II DNA Labeling Kit (Ambion#1455). CENTRI-SEP Columns from Princeton Separations (#CS-900) was used for probe purification. The blots were prehybridized in ExpressHyb solution (Clontech #8015-

1) at 68°C for 1 hour, and hybridized at 68°C for 2 hours. Wash conditions were 2xSSC, 0.05%SDS at room temperature for 30 minutes and twice in 0.1xSSC, 0.1%SDS at 50°C for 20 minutes per wash. The blot was exposed overnight on a PhosphorImager (Storm, Molecular Dynamics) at room temperature and analyzed using the Molecular Dynamics ImageQuant software. Northern analysis showed a single band of approximately 3.0 kb, expressed at a high level in CNS (medulla oblongata) and non-CNS (ovary); medium level in CNS (caudate nucleus, putamen, thalamus, substantia nigra, spinal cord) and non-CNS (testis) and low level in CNS (amygdala, hippocampus, subthalamic nucleus, cerebral cortex, occipital pole, frontal lobe, temporal lobe, cerebellum, corpus callosum) and non-CNS (thymus, prostate, skeletal muscle, kidney, pancreas, heart), as shown in Figure 3A-D.

WHAT IS CLAIMED IS:

1. A purified nucleic acid molecule encoding a human endothelin converting enzyme-3 protein which comprises the nucleotide sequence:

5 GGC GGCGGGC GCTGGGAGAC ACCGGACGCC CGCTCGGCTG CGCTGCGGCT CAGGCCCCCG
CYCGGGCCCG ACCCGCTCGG TCACCGCCCG CTCGGGCGCG CACCTGCCCG CTGCGGCCCG
AGGGCCATGC GGAGGCCAC GAGGAGGCCG GCGGCCACGC GCATCCCGTA GCCAGGTGG
CCCAGGTCTG CACCGCGGCG GCCTCGGCGC CATGGAGCCC CCGTATTCGC TGACGGCGCA
CTACGATGAG TTCCAAGAGG TCAAGTACGT GAGCCGCTGC GGCGCGGGG GCGCGCGCGG
10 GGCCTCCCTG CCCCCGGGCT TCCCGTTGGG CGCTGCCCCG AGCGCCACCG GGGCCCGGTC
CGGGCTGCCG CGCTGGAACC GGCGCGAGGT GTGCCTGCTG TCGGGGCTGG GTTTCGCCCG
CGGCCTCTGC GCCATTCTGG CGGCTATGCT GGCCCTCAAG TACCTGGGCC CGGTGCGGGC
CGGCGGCGGC GCCTGTCCCG AGGGCTGCCC TGAGCGCAAG GCCTTCGCGC GCGCCGCTCG
CTTCCTGGCC GCCAACCTGG ACGCCAGCAT CGACCCATGC CAGGACTTCT ACTCGTTCGC
15 CTGCGGCGGT TGGCTGCGGC GCCACGCCAT CCCCACGAC AAGCTCACCT ATGGCACCAT
CGCGGCCATC GGCGAGCAA ACGAGGAGCG CCTACGGCGC CTGCTGGCGC GGCCCGGGGG
TGGGCTTGGC GGCGCGGGCC AGCGCAAGGT GCGCGCCTTC TTCCGCTCGT GCCTCGACAT
GCGCGAGATC GAGCGACTGG GCGCGGACC CATGCTAGAG GTCATCGAGG ACTGCGGGGG
CTGGGACCTG GGCGGCGCGG AGGAGCGTCC GGGGTCGCG GCGCGATGGG ACCTCAACCG
20 GCTGCTGTAC AAGGCGCAGG GCGTGTACAG CGCCGCCGCG CTCTTCTCGC TCACGGTCAG
CCTGGACGAC AGGAACTCCT CGCGCTACGT CATCCGCATT GACCAGGATG GGCTCACCT
GCCAGAGAGG ACCCTGTACC TCGCTCAGGA TGAGGACAGT GAGAAGATCC TGGCAGCATA
CAGGGTGTTC ATGGAGCGAG TGCTCAGCCT CCTGGGTGCA GACGCTGTGG AACAGAAGGC
CCAAGAGATC CTGCAAGTGG AGCAGCAGCT GGCCAACATC ACTGTGTCAG AGTATGACGA
25 CCTACGGCGA GATGTCAGCT CCATGTACAA CAAGGTGACG CTGGGGCAGC TGCAGAAGAT
CACCCCCAC TTGCGGTGGA AGTGGCTGCT AGACCAGATC TTCCAGGAGG ACTTCTCAGA
GGAAGAGGAG GTGGTGCTGC TGGCGACAGA CTACATGCAG CAGGTGTCGC AGCTCATCCG
CTCCACACCC CACCGGTCC TGCACAACTA CCTGGTGTGG CGCGTGGTGG TGGTCTGAG
TGAACACCTG TCCCCGCCAT TCCGTGAGGC ACTGCACGAG CTGGCACAGG AGATGGAGGG
30 CAGCGACAAG CCACAGGAGC TGGCCCGGGT CTGCTTGGGC CAGGCCAATC GCCACTTTGG
CATGGCGCTT GGCGCCCTCT TTGTACATGA GCACTTCTCA GCTGCCAGCA AAGCCAAGGT
GCAGCAGCTA GTGGAAGACA TCAAGTACAT CCTGGGCCAG CGCCTGGAGG AGCTGGACTG
GATGGACGCC GAGACCAGGG CTGCTGCTCG GGCCAAGCTC CAGTACATGA TGGTGATGGT
CGGCTACCCG GACTTCCTGC TGAAACCCGA TGCTGTGGAC AAGGAGTATG AGTTGAGGT

CCATGAGAAG ACCTACTTCA AGAACATCTT GAACAGCATC CGCTTCAGCA TCCAGCTCTC
 AGTTAAGAAG ATTTCGGCAGG AGGTGGACAA GTCCACGTGG CTGCTCCCCC CACAGGCGCT
 CAATGCCTAC TATCTACCCA ACAAGAACCA GATGGTGTTC CCCGCGGGCA TCCTGCAGCC
 CACCCTGTAC GACCCTGACT TCCCACAGTC TCTCAACTAC GGGGGCATCG GCACCATCAT
 5 TGGACATGAG CTGACCCACG GCTACGACGA CTGGGGGGGC CAGTATGACC GCTCAGGGAA
 CCTGCTGCAC TGGTGGACGG AGGCCTCCTA CAGCCGCTTC CTGCGAAAGG CTGAGTGCAT
 CGTCCGTCTC TATGACAACT TCACTGTCTA CAACCAGCGG GTGAACGGGA AACACACGCT
 TGGGGAGAAC ATCGCAGATA TGGGCGGCCT CAAGCTGGCC TACCACGCCT ATCAGAAGTG
 GGTGCGGGAG CACGGCCCAG AGCACCCACT TCCCCGGCTC AAGTACACAC ATGACCAGCT
 10 CTTCTTCATT GCCTTTGCCC AGAACTGGTG CATCAAGCGG CGGTCGCAGT CCATCTACCT
 GCAGGTGCTG ACTGACAAGC ATGCCCCCTGA GCACTACAGG GTGCTGGGCA GTGTGTCCCA
 GTTTGAGGAG TTTGGCCGGG CTTTCCACTG TCCCAAGGAC TCACCCATGA ACCCTGCCCA
 CAAGTGTTCC GTGTGGTGAG CCTGGCTGCC CGCCTGCACG CCCCCACTGC CCCCACGCA
 ATCACCTCCT GCTGGCTACC GGGGCAGGCA TGCACCCGGT GCCAGCCCCG CTCTGGGCAC
 15 CACCTGCCTT CCAGCCCCTC CAGGACCCCG TCCCCCTGCT GCCCCTCACT TCAGGAGGGG
 CCTGGAGCAG GGTGAGGCTG GACTTTGGGG GGCTGTGAGG GAAATATACT GGGGTCCCCA
 GATTCTGCTC TAAGGGGGCC AGACCCTCTG CCAGGCTGGA TTGTACGGGC CCCACCTTCG
 CTGTGTTCTT GCTGCAAAGT CTGGTCAATA AATCACTGCA CTGTAAAAA AAAAAAAAAA
 AAAAAATTCC TGCG (SEQ ID NO:1).

20

2. A purified DNA molecule encoding human endothelin
 converting enzyme-3 protein wherein said DNA molecule encodes a protein
 comprising the amino acid sequence:

Met Glu Pro Pro Tyr Ser Leu Thr Ala His Tyr Asp Glu Phe Gln Glu
 25 Val Lys Tyr Val Ser Arg Cys Gly Ala Gly Gly Ala Arg Gly Ala Ser
 Leu Pro Pro Gly Phe Pro Leu Gly Ala Ala Arg Ser Ala Thr Gly Ala
 Arg Ser Gly Leu Pro Arg Trp Asn Arg Arg Glu Val Cys Leu Leu Ser
 Gly Leu Val Phe Ala Ala Gly Leu Cys Ala Ile Leu Ala Ala Met Leu
 Ala Leu Lys Tyr Leu Gly Pro Val Ala Ala Gly Gly Gly Ala Cys Pro
 30 Glu Gly Cys Pro Glu Arg Lys Ala Phe Ala Arg Ala Ala Arg Phe Leu
 Ala Ala Asn Leu Asp Ala Ser Ile Asp Pro Cys Gln Asp Phe Tyr Ser
 Phe Ala Cys Gly Gly Trp Leu Arg Arg His Ala Ile Pro Asp Asp Lys
 Leu Thr Tyr Gly Thr Ile Ala Ala Ile Gly Glu Gln Asn Glu Glu Arg
 Leu Arg Arg Leu Leu Ala Arg Pro Gly Gly Gly Pro Gly Gly Ala Ala

Gln Arg Lys Val Arg Ala Phe Phe Arg Ser Cys Leu Asp Met Arg Glu
 Ile Glu Arg Leu Gly Pro Arg Pro Met Leu Glu Val Ile Glu Asp Cys
 Gly Gly Trp Asp Leu Gly Gly Ala Glu Glu Arg Pro Gly Val Ala Ala
 Arg Trp Asp Leu Asn Arg Leu Leu Tyr Lys Ala Gln Gly Val Tyr Ser
 5 Ala Ala Ala Leu Phe Ser Leu Thr Val Ser Leu Asp Asp Arg Asn Ser
 Ser Arg Tyr Val Ile Arg Ile Asp Gln Asp Gly Leu Thr Leu Pro Glu
 Arg Thr Leu Tyr Leu Ala Gln Asp Glu Asp Ser Glu Lys Ile Leu Ala
 Ala Tyr Arg Val Phe Met Glu Arg Val Leu Ser Leu Leu Gly Ala Asp
 Ala Val Glu Gln Lys Ala Gln Glu Ile Leu Gln Val Glu Gln Gln Leu
 10 Ala Asn Ile Thr Val Ser Glu Tyr Asp Asp Leu Arg Arg Asp Val Ser
 Ser Met Tyr Asn Lys Val Thr Leu Gly Gln Leu Gln Lys Ile Thr Pro
 His Leu Arg Trp Lys Trp Leu Leu Asp Gln Ile Phe Gln Glu Asp Phe
 Ser Glu Glu Glu Glu Val Val Leu Leu Ala Thr Asp Tyr Met Gln Gln
 Val Ser Gln Leu Ile Arg Ser Thr Pro His Arg Val Leu His Asn Tyr
 15 Leu Val Trp Arg Val Val Val Val Leu Ser Glu His Leu Ser Pro Pro
 Phe Arg Glu Ala Leu His Glu Leu Ala Gln Glu Met Glu Gly Ser Asp
 Lys Pro Gln Glu Leu Ala Arg Val Cys Leu Gly Gln Ala Asn Arg His
 Phe Gly Met Ala Leu Gly Ala Leu Phe Val His Glu His Phe Ser Ala
 Ala Ser Lys Ala Lys Val Gln Gln Leu Val Glu Asp Ile Lys Tyr Ile
 20 Leu Gly Gln Arg Leu Glu Glu Leu Asp Trp Met Asp Ala Glu Thr Arg
 Ala Ala Ala Arg Ala Lys Leu Gln Tyr Met Met Val Met Val Gly Tyr
 Pro Asp Phe Leu Leu Lys Pro Asp Ala Val Asp Lys Glu Tyr Glu Phe
 Glu Val His Glu Lys Thr Tyr Phe Lys Asn Ile Leu Asn Ser Ile Arg
 Phe Ser Ile Gln Leu Ser Val Lys Lys Ile Arg Gln Glu Val Asp Lys
 25 Ser Thr Trp Leu Leu Pro Pro Gln Ala Leu Asn Ala Tyr Tyr Leu Pro
 Asn Lys Asn Gln Met Val Phe Pro Ala Gly Ile Leu Gln Pro Thr Leu
 Tyr Asp Pro Asp Phe Pro Gln Ser Leu Asn Tyr Gly Gly Ile Gly Thr
 Ile Ile Gly His Glu Leu Thr His Gly Tyr Asp Asp Trp Gly Gly Gln
 Tyr Asp Arg Ser Gly Asn Leu Leu His Trp Trp Thr Glu Ala Ser Tyr
 30 Ser Arg Phe Leu Arg Lys Ala Glu Cys Ile Val Arg Leu Tyr Asp Asn
 Phe Thr Val Tyr Asn Gln Arg Val Asn Gly Lys His Thr Leu Gly Glu
 Asn Ile Ala Asp Met Gly Gly Leu Lys Leu Ala Tyr His Ala Tyr Gln
 Lys Trp Val Arg Glu His Gly Pro Glu His Pro Leu Pro Arg Leu Lys
 Tyr Thr His Asp Gln Leu Phe Phe Ile Ala Phe Ala Gln Asn Trp Cys

Ile Lys Arg Arg Ser Gln Ser Ile Tyr Leu Gln Val Leu Thr Asp Lys
His Ala Pro Glu His Tyr Arg Val Leu Gly Ser Val Ser Gln Phe Glu
Glu Phe Gly Arg Ala Phe His Cys Pro Lys Asp Ser Pro Met Asn Pro
Ala His Lys Cys Ser Val Trp (SEQ ID NO:2).

5

3. An expression vector for the expression of an endothelin
converting enzyme-3 in a recombinant host cell wherein said expression vector
comprises a DNA molecule which encodes the amino acid sequence of claim 2.

10

4. An expression vector of claim 3 which is a eukaryotic
expression vector.

15

5. An expression vector of claim 3 which is a prokaryotic
expression vector.

20

6. A host cell which expresses a recombinant endothelin
converting enzyme-3 protein wherein said host cell contains the expression vector of
claim 3.

7. A host cell which expresses a recombinant endothelin
converting enzyme-3 wherein said host cell contains the expression vector of claim 4.

25

8. A host cell which expresses a recombinant endothelin
converting enzyme-3 protein wherein said host cell contains the expression vector of
claim 5.

30

9. A subcellular membrane fraction obtained from the host cell of
claim 6 which contains recombinant endothelin converting enzyme-3.

10. A subcellular membrane fraction obtained from the host cell of
claim 7 which contains recombinant endothelin converting enzyme-3.

11. A subcellular membrane fraction obtained from the host cell of
claim 8 which contains recombinant endothelin converting enzyme-3.

12. A purified DNA molecule encoding endothelin converting enzyme-3 which consists of the nucleotide sequence:

```
GGCGGCGGGC GCTGGGAGAC ACCGGACGCC CGCTCGGCTG CGCTGCGGCT CAGGCCCCCG
5  CYCGGGCCCCG ACCCGCTCGG TCACCGCCGG CTCGGGCGCG CACCTGCCGG CTGCGGCCCC
AGGGCCATGC GGAGGCCAC GAGGAGGCCG GCGGCCACGC GCATCCCGTA GCCAGGTGG
CCCAGGTCTG CACCGCGGCG GCCTCGGCGC CATGGAGCCC CCGTATTGCG TGACGGCGCA
CTACGATGAG TTCCAAGAGG TCAAGTACGT GAGCCGCTGC GGCGCGGGGG GCGCGCGCGG
GGCCTCCCTG CCCCCGGGCT TCCCGTTGGG CGCTGCCCGC AGCGCCACCG GGGCCCGGTC
10 CGGGCTGCCG CGCTGGAACC GGCGCGAGGT GTGCCTGCTG TCGGGGCTGG TGTTCCGCGC
CGGCCTCTGC GCCATTCTGG CGGCTATGCT GGCCCTCAAG TACCTGGGCC CGGTGCGGGC
CGGCGGCGGC GCCTGTCCCG AGGGCTGCCC TGAGCGCAAG GCCTTCGCGC GCGCCGCTCG
CTTCTTGCC GCCAACCTGG ACGCCAGCAT CGACCCATGC CAGGACTTCT ACTCGTTCGC
CTGCGGCGGT TGGCTGCGGC GCCACGCCAT CCCCAGCGAC AAGCTCACCT ATGGCACCAT
15 CGCGGCCATC GGCGAGCAA ACGAGGAGCG CTTACGGCGC CTGCTGGCGC GGCCCGGGGG
TGGGCCTGGC GGCGCGGCC AGCGCAAGGT GCGCGCCTTC TTCCGCTCGT GCCTCGACAT
GCGCGAGATC GAGCGACTGG GCGCGGACC CATGCTAGAG GTCATCGAGG ACTGCGGGGG
CTGGGACCTG GGCGGCGCGG AGGAGCGTCC GGGGGTCGCG GCGCGATGGG ACCTCAACCG
GCTGCTGTAC AAGGCGCAGG GCGGTACAG CGCCGCCGCG CTCTTCTCGC TCACGGTCAG
20 CCTGGACGAC AGGAACCTCT CGCGCTACGT CATCCGCATT GACCAGGATG GGCTCACCTT
GCCAGAGAGG ACCCTGTACC TCCTCAGGA TGAGGACAGT GAGAAGATCC TGGCAGCATA
CAGGGTGTTT ATGGAGCGAG TGCTCAGCCT CCTGGGTGCA GACGCTGTGG AACAGAAGGC
CCAAGAGATC CTGCAAGTGG AGCAGCAGCT GGCCAACATC ACTGTGTCAG AGTATGACGA
CCTACGGCGA GATGTCAGCT CCATGTACAA CAAGGTGACG CTGGGGCAGC TGCAGAAGAT
25 CACCCCCAC TTGCGGTGGA AGTGGCTGCT AGACCAGATC TTCCAGGAGG ACTTCTCAGA
GGAAGAGGAG GTGGTGCTGC TGGCGACAGA CTACATGCAG CAGGTGTCGC AGCTCATCCG
CTCCACACCC CACCGGGTCC TGCACAATA CCTGGTGTGG CGCGTGGTGG TGGTCCTGAG
TGAACACCTG TCCCCGCCAT TCCGTGAGGC ACTGCACGAG CTGGCACAGG AGATGGAGGG
CAGCGACAAG CCACAGGAGC TGGCCCGGGT CTGCTTGGGC CAGGCCAATC GCCACTTTGG
30 CATGGCGCTT GGCGCCCTCT TTGTACATGA GCACTTCTCA GCTGCCAGCA AAGCCAAGGT
GCAGCAGCTA GTGGAAGACA TCAAGTACAT CCTGGGCCAG CGCCTGGAGG AGCTGGACTG
GATGGACGCC GAGACCAGGG CTGCTGCTCG GGCCAAGCTC CAGTACATGA TGGTGATGGT
CGGCTACCCG GACTTCCTGC TGAAACCCGA TGCTGTGGAC AAGGAGTATG AGTTTGAGGT
CCATGAGAAG ACCTACTTCA AGAACATCTT GAACAGCATC CGCTTCAGCA TCCAGCTCTC
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AGTTAAGAAG ATTCGGCAGG AGGTGGACAA GTCCACGTGG CTGCTCCCCC CACAGGCGCT
 CAATGCCTAC TATCTACCCA ACAAGAACCA GATGGTGTTT CCCGCGGGCA TCCTGCAGCC
 CACCCTGTAC GACCCCTGACT TCCCACAGTC TCTCAACTAC GGGGGCATCG GCACCATCAT
 TGGACATGAG CTGACCCACG GCTACGACGA CTGGGGGGGC CAGTATGACC GCTCAGGGAA
 5 CCTGCTGCAC TGGTGGACGG AGGCCTCCTA CAGCCGCTTC CTGCGAAAGG CTGAGTGCAT
 CGTCCGTCTC TATGACAAC TCACTGTCTA CAACCAGCGG GTGAACGGGA AACACACGCT
 TGGGGAGAAC ATCGCAGATA TGGGCGGCCT CAAGCTGGCC TACCACGCCT ATCAGAAGTG
 GGTGCGGGAG CACGGCCCAG AGCACCCACT TCCCCGGCTC AAGTACACAC ATGACCAGCT
 CTTCTTCATT GCCTTTGCCC AGAACTGGTG CATCAAGCGG CGGTCGCACT CCATCTACCT
 10 GCAGGTGCTG ACTGACAAGC ATGCCCCCTGA GCACTACAGG GTGCTGGGCA GTGTGTCCCA
 GTTTGAGGAG TTTGGCCGGG CTTTCCACTG TCCCAAGGAC TCACCCATGA ACCCTGCCCA
 CAAGTGTTC GTGTGGTGAG CCTGGCTGCC CGCCTGCACG CCCCCACTGC CCCCACACGA
 ATCACCTCCT GCTGGCTACC GGGGCAGGCA TGCACCCGGT GCCAGCCCCG CTCTGGGCAC
 CACCTGCCTT CCAGCCCCCTC CAGGACCCGG TCCCCCTGCT GCCCCCTCACT TCAGGAGGGG
 15 CCTGGAGCAG GGTGAGGCTG GACTTTGGGG GGCTGTGAGG GAAATATACT GGGGTCCCCA
 GATTCTGCTC TAAGGGGGCC AGACCCTCTG CCAGGCTGGA TTGTACGGGC CCCACCTTCG
 CTGTGTTCTT GCTGCAAAGT CTGGTCAATA AATCACTGCA CTGTTAAAAA AAAAAAAAAA
 AAAAAATTCC TGCG (SEQ ID NO:1).

20 13. The purified DNA molecule of claim 12 which consists of a nucleotide sequence from nucleotide 212 to nucleotide 2539 of SEQ ID NO:1.

 14. An expression vector for the expression of endothelin
 converting enzyme-3 in a recombinant host cell wherein said expression vector
 25 comprises a DNA molecule of claim 13.

15 15. An expression vector of claim 14 which is a eukaryotic expression vector.

30 16. An expression vector of claim 14 which is a prokaryotic expression vector.

17. A host cell which expresses a recombinant endothelin converting enzyme-3 wherein said host cell contains the expression vector of claim 14.

5 18. A host cell which expresses a recombinant endothelin converting enzyme-3 wherein said host cell contains the expression vector of claim 15.

10 19. A host cell which expresses a recombinant endothelin converting enzyme-3 wherein said host cell contains the expression vector of claim 16.

15 20. A subcellular membrane fraction obtained from the host cell of claim 17 which contains recombinant endothelin converting enzyme-3.

21. A subcellular membrane fraction obtained from the host cell of claim 18 which contains recombinant endothelin converting enzyme-3.

20 22. A subcellular membrane fraction obtained from the host cell of claim 19 which contains recombinant endothelin converting enzyme-3.

23. A purified endothelin converting enzyme-3 protein which comprises the amino acid sequence:

Met Glu Pro Pro Tyr Ser Leu Thr Ala His Tyr Asp Glu Phe Gln Glu
25 Val Lys Tyr Val Ser Arg Cys Gly Ala Gly Gly Ala Arg Gly Ala Ser
Leu Pro Pro Gly Phe Pro Leu Gly Ala Ala Arg Ser Ala Thr Gly Ala
Arg Ser Gly Leu Pro Arg Trp Asn Arg Arg Glu Val Cys Leu Leu Ser
Gly Leu Val Phe Ala Ala Gly Leu Cys Ala Ile Leu Ala Ala Met Leu
Ala Leu Lys Tyr Leu Gly Pro Val Ala Ala Gly Gly Gly Ala Cys Pro
30 Glu Gly Cys Pro Glu Arg Lys Ala Phe Ala Arg Ala Ala Arg Phe Leu
Ala Ala Asn Leu Asp Ala Ser Ile Asp Pro Cys Gln Asp Phe Tyr Ser
Phe Ala Cys Gly Gly Trp Leu Arg Arg His Ala Ile Pro Asp Asp Lys
Leu Thr Tyr Gly Thr Ile Ala Ala Ile Gly Glu Gln Asn Glu Glu Arg
Leu Arg Arg Leu Leu Ala Arg Pro Gly Gly Gly Pro Gly Gly Ala Ala

Gln Arg Lys Val Arg Ala Phe Phe Arg Ser Cys Leu Asp Met Arg Glu
Ile Glu Arg Leu Gly Pro Arg Pro Met Leu Glu Val Ile Glu Asp Cys
Gly Gly Trp Asp Leu Gly Gly Ala Glu Glu Arg Pro Gly Val Ala Ala
Arg Trp Asp Leu Asn Arg Leu Leu Tyr Lys Ala Gln Gly Val Tyr Ser
5 Ala Ala Ala Leu Phe Ser Leu Thr Val Ser Leu Asp Asp Arg Asn Ser
Ser Arg Tyr Val Ile Arg Ile Asp Gln Asp Gly Leu Thr Leu Pro Glu
Arg Thr Leu Tyr Leu Ala Gln Asp Glu Asp Ser Glu Lys Ile Leu Ala
Ala Tyr Arg Val Phe Met Glu Arg Val Leu Ser Leu Leu Gly Ala Asp
Ala Val Glu Gln Lys Ala Gln Glu Ile Leu Gln Val Glu Gln Gln Leu
10 Ala Asn Ile Thr Val Ser Glu Tyr Asp Asp Leu Arg Arg Asp Val Ser
Ser Met Tyr Asn Lys Val Thr Leu Gly Gln Leu Gln Lys Ile Thr Pro
His Leu Arg Trp Lys Trp Leu Leu Asp Gln Ile Phe Gln Glu Asp Phe
Ser Glu Glu Glu Glu Val Val Leu Leu Ala Thr Asp Tyr Met Gln Gln
Val Ser Gln Leu Ile Arg Ser Thr Pro His Arg Val Leu His Asn Tyr
15 Leu Val Trp Arg Val Val Val Val Leu Ser Glu His Leu Ser Pro Pro
Phe Arg Glu Ala Leu His Glu Leu Ala Gln Glu Met Glu Gly Ser Asp
Lys Pro Gln Glu Leu Ala Arg Val Cys Leu Gly Gln Ala Asn Arg His
Phe Gly Met Ala Leu Gly Ala Leu Phe Val His Glu His Phe Ser Ala
Ala Ser Lys Ala Lys Val Gln Gln Leu Val Glu Asp Ile Lys Tyr Ile
20 Leu Gly Gln Arg Leu Glu Glu Leu Asp Trp Met Asp Ala Glu Thr Arg
Ala Ala Ala Arg Ala Lys Leu Gln Tyr Met Met Val Met Val Gly Tyr
Pro Asp Phe Leu Leu Lys Pro Asp Ala Val Asp Lys Glu Tyr Glu Phe
Glu Val His Glu Lys Thr Tyr Phe Lys Asn Ile Leu Asn Ser Ile Arg
Phe Ser Ile Gln Leu Ser Val Lys Lys Ile Arg Gln Glu Val Asp Lys
25 Ser Thr Trp Leu Leu Pro Pro Gln Ala Leu Asn Ala Tyr Tyr Leu Pro
Asn Lys Asn Gln Met Val Phe Pro Ala Gly Ile Leu Gln Pro Thr Leu
Tyr Asp Pro Asp Phe Pro Gln Ser Leu Asn Tyr Gly Gly Ile Gly Thr
Ile Ile Gly His Glu Leu Thr His Gly Tyr Asp Asp Trp Gly Gly Gln
Tyr Asp Arg Ser Gly Asn Leu Leu His Trp Trp Thr Glu Ala Ser Tyr
30 Ser Arg Phe Leu Arg Lys Ala Glu Cys Ile Val Arg Leu Tyr Asp Asn
Phe Thr Val Tyr Asn Gln Arg Val Asn Gly Lys His Thr Leu Gly Glu
Asn Ile Ala Asp Met Gly Gly Leu Lys Leu Ala Tyr His Ala Tyr Gln
Lys Trp Val Arg Glu His Gly Pro Glu His Pro Leu Pro Arg Leu Lys
Tyr Thr His Asp Gln Leu Phe Phe Ile Ala Phe Ala Gln Asn Trp Cys

Ile Lys Arg Arg Ser Gln Ser Ile Tyr Leu Gln Val Leu Thr Asp Lys
His Ala Pro Glu His Tyr Arg Val Leu Gly Ser Val Ser Gln Phe Glu
Glu Phe Gly Arg Ala Phe His Cys Pro Lys Asp Ser Pro Met Asn Pro
Ala His Lys Cys Ser Val Trp (SEQ ID NO:2).

5

24. The purified endothelin converting enzyme-3 protein of claim 23 which consists of the amino acid sequence as set forth in SEQ ID NO:2.

25. A process for the expression of an endothelin converting
10 enzyme-3 in a recombinant host cell, comprising:
(a) transfecting the expression vector of claim 3 into a suitable host cell; and,
(b) culturing the host cells of step (a) under conditions which allow expression of the endothelin converting enzyme-3 protein from the expression
15 vector.

26. A method for determining whether a substance is capable of binding to endothelin converting enzyme-3 comprising:
(a) providing test cells by transfecting cells with an expression
20 vector that directs the expression of endothelin converting enzyme-3 as set forth as SEQ ID NO:2 in the cells;
(b) exposing the test cells to the substance;
(c) measuring the amount of binding of the substance to the endothelin converting enzyme-3;
25 (d) comparing the amount of binding of the substance to the endothelin converting enzyme-3 in the test cells with the amount of binding of the substance to control cells that have not been transfected with the expression vector that directs the expression of endothelin converting enzyme-3 as set forth as SEQ ID NO:2.

30

27. A method for determining whether a substance is capable of modulating endothelin converting enzyme-3 activity comprising:

(a) providing test cells by transfecting cells with an expression vector that directs the expression of endothelin converting enzyme-3 as set forth as SEQ ID NO:2;

(b) exposing the test cells to the substance;

5 (c) measuring the amount of an accumulated intracellular secondary message;

(d) comparing the amount of the secondary message in the test cells in response to the substance with the amount of secondary message in test cells that have not been exposed to the substance.

10

28. The method of claim 27 wherein the secondary message is cAMP.

29. A method for determining whether a substance is capable of
15 modulating endothelin converting enzyme-3 activity comprising:

(a) providing test cells by transfecting cells with an expression vector that directs the expression of endothelin converting enzyme-3 as set forth as SEQ ID NO:2;

(b) purifying membrane preparations comprising the endothelin
20 converting enzyme-3;

(c) adding a test substance to the purified membrane preparations of step (b);

(d) incubating the test substance-containing membrane preparation of step (c) with a substrate of endothelin converting enzyme-3;

25 (e) comparing the product generated from step (d) versus the amount of product generated from a membrane preparation containing the substrate of step (d) without addition of the test substance of step (c).

30. The method of claim 29 wherein the substrate is selected from
30 the group consisting of big ET-1, big ET-2 and big ET-3.

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GGCGGCGGGC GCTGGGAGAC ACCGGACGCC CGCTCGGCTG CGCTGCGGCT CAGGCCCCCG
CTCGGGCCCCG ACCCGCTCGG TCACCGCCGG CTCGGGCGCG CACCTGCCGG CTGCGGCCCC
AGGGCCATGC GGAGGCCAC GAGGAGGCCG GCGGCCACGC GCATCCCGTA GCCCAGGTGG
CCCAGGTCTG CACCGCGGCG GCCTCGGCGC CATGGAGCCC CCGTATTCGC TGACGGCGCA
CTACGATGAG TTCCAAGAGG TCAAGTACGT GAGCCGCTGC GGC GCGGGGG GCGCGCGCGG
GGCCTCCCTG CCCCCGGGCT TCCCGTTGGG CGCTGCCCGC AGCGCCACCG GGGCCCGGTC
CGGGCTGCCG CGCTGGAACC GGC GCGAGGT GTGCCTGCTG TCGGGGCTGG TGTTCGCCGC
CGGCCTCTGC GCCATTCTGG CGGCTATGCT GGCCCTCAAG TACCTGGGCC CGGTGCGGGC
CGGCGGCGGC GCCTGTCCCG AGGGCTGCCC TGAGCGCAAG GCCTTCGCGC GCGCCGCTCG
CTTCCTGGCC GCCAACCTGG ACGCCAGCAT CGACCCATGC CAGGACTTCT ACTCGTTCGC
CTGCGGCGGT TGGCTGCGGC GCCACGCCAT CCCC GACGAC AAGCTCACCT ATGGCACCAT
CGCGGCCATC GGC GAGCAAA ACGAGGAGCG CCTACGGCGC CTGCTGGCGC GGGCCGGGGG
TGGGCCTGGC GGC GCGGGCC AGCGCAAGGT GCGCGCCTTC TTCCGCTCGT GCCTCGACAT
GCGCGAGATC GAGCGACTGG GCGCGGACC CATGCTAGAG GTCATCGAGG ACTGCGGGGG
CTGGGACCTG GGC GCGCGCG AGGAGCGTCC GGGGGTCGCG GCGCGATGGG ACCTCAACCG
GCTGCTGTAC AAGGCGCAGG GCGTGTACAG CGCCGCCGCG CTCTTCTCGC TCACGGTCAG
CCTGGACGAC AGGAACTCCT CGCGCTACGT CATCCGCATT GACCAGGATG GGCTCACCCCT
GCCAGAGAGG ACCCTGTACC TCGCTCAGGA TGAGGACAGT GAGAAGATCC TGGCAGCATA
CAGGGTGTTT ATGGAGCGAG TGCTCAGCCT CCTGGGTGCA GACGCTGTGG AACAGAAGGC
CCAAGAGATC CTGCAAGTGG AGCAGCAGCT GGCCAACATC ACTGTGTCAG AGTATGACGA
CCTACGGCGA GATGTCAGCT CCATGTACAA CAAGGTGACG CTGGGGCAGC TGCAGAAGAT
CACCCCCAC TTGCGGTGGA AGTGGCTGCT AGACCAGATC TTCCAGGAGG ACTTCTCAGA
GGAAGAGGAG GTGGTGCTGC TGGCGACAGA CTACATGCAG CAGGTGTGCG AGTCATCCG
CTCCACACCC CACCGGGTCC TGCACAACTA CCTGGTGTGG CGCGTGGTGG TGGTCCTGAG
TGAACACCTG TCCCCGCCAT TCCGTGAGGC ACTGCACGAG CTGGCACAGG AGATGGAGGG
CAGCGACAAG CCACAGGAGC TGGCCCGGGT CTGCTTGGGC CAGGCCAATC GCCACTTTGG

FIG. 1A

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CATGGCGCTT GGC GCCCTCT TTGTACATGA GCACTTCTCA GCTGCCAGCA AAGCCAAGGT
GCAGCAGCTA GTGGAAGACA TCAAGTACAT CCTGGGCCAG CGCCTGGAGG AGCTGGACTG
GATGGACGCC GAGACCAGGG CTGCTGCTCG GGCCAAGCTC CAGTACATGA TGGTGATGGT
CGGCTACCCG GACTTCCTGC TGAAACCCGA TGCTGTGGAC AAGGAGTATG AGTTTGAGGT
CCATGAGAAG ACCTACTTCA AGAACATCTT GAACAGCATC CGCTTCAGCA TCCAGCTCTC
AGTTAAGAAG ATTCGGCAGG AGGTGGACAA GTCCACGTGG CTGCTCCCCC CACAGGCGCT
CAATGCCTAC TATCTACCCA ACAAGAACCA GATGGTGTTT CCCGCGGGCA TCCTGCAGCC
CACCTGTAC GACCCTGACT TCCCACAGTC TCTCAACTAC GGGGGCATCG GCACCATCAT
TGGACATGAG CTGACCCACG GCTACGACGA CTGGGGGGGC CAGTATGACC GCTCAGGGAA
CCTGCTGCAC TGGTGGACGG AGGCCTCCTA CAGCCGCTTC CTGCGAAAGG CTGAGTGCAT
CGTCCGTCTC TATGACAACT TCACTGTCTA CAACCAGCGG GTGAACGGGA AACACACGCT
TGGGGAGAAC ATCGCAGATA TGGGCGGCCT CAAGCTGGCC TACCACGCCT ATCAGAAGTG
GGTGCGGGAG CACGGCCCAG AGCACCCACT TCCCCGGCTC AAGTACACAC ATGACCAGCT
CTTCTTCATT GCCTTTGCCC AGAACTGGTG CATCAAGCGG CGGTGCGAGT CCATCTACCT
GCAGGTGCTG ACTGACAAGC ATGCCCTGA GCACTACAGG GTGCTGGGCA GTGTGTCCCA
GTTTGAGGAG TTTGGCCGGG CTTTCCACTG TCCCAAGGAC TCACCCATGA ACCCTGCCCA
CAAGTGTTC GTGTGGTGAG CCTGGCTGCC CGCCTGCACG CCCCCACTGC CCCCACGCA
ATCACCTCCT GCTGGCTACC GGGGCAGGCA TGCACCCGGT GCCAGCCCCG CTCTGGGCAC
CACCTGCCTT CCAGCCCCTC CAGGACCCGG TCCCCCTGCT GCCCTCACT TCAGGAGGGG
CCTGGAGCAG GGTGAGGCTG GACTTTGGGG GGCTGTGAGG GAAATATACT GGGGTCCCCA
GATTCTGCTC TAAGGGGGCC AGACCCTCTG CCAGGCTGGA TTGTACGGGC CCCACCTTCG
CTGTGTTCTT GCTGCAAAGT CTGGTCAATA AATCACTGCA CTGTTAAAAA AAAAAAAAAA
AAAAAATTCC TGCG (SEQ ID NO:1)

FIG. 1B

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Met Glu Pro Pro Tyr Ser Leu Thr Ala His Tyr Asp Glu Phe Gln Glu
Val Lys Tyr Val Ser Arg Cys Gly Ala Gly Gly Ala Arg Gly Ala Ser
Leu Pro Pro Gly Phe Pro Leu Gly Ala Ala Arg Ser Ala Thr Gly Ala
Arg Ser Gly Leu Pro Arg Trp Asn Arg Arg Glu Val Cys Leu Leu Ser
Gly Leu Val Phe Ala Ala Gly Leu Cys Ala Ile Leu Ala Ala Met Leu
Ala Leu Lys Tyr Leu Gly Pro Val Ala Ala Gly Gly Gly Ala Cys Pro
Glu Gly Cys Pro Glu Arg Lys Ala Phe Ala Arg Ala Ala Arg Phe Leu
Ala Ala Asn Leu Asp Ala Ser Ile Asp Pro Cys Gln Asp Phe Tyr Ser
Phe Ala Cys Gly Gly Trp Leu Arg Arg His Ala Ile Pro Asp Asp Lys
Leu Thr Tyr Gly Thr Ile Ala Ala Ile Gly Glu Gln Asn Glu Glu Arg
Leu Arg Arg Leu Leu Ala Arg Pro Gly Gly Gly Pro Gly Gly Ala Ala
Gln Arg Lys Val Arg Ala Phe Phe Arg Ser Cys Leu Asp Met Arg Glu
Ile Glu Arg Leu Gly Pro Arg Pro Met Leu Glu Val Ile Glu Asp Cys
Gly Gly Trp Asp Leu Gly Gly Ala Glu Glu Arg Pro Gly Val Ala Ala
Arg Trp Asp Leu Asn Arg Leu Leu Tyr Lys Ala Gln Gly Val Tyr Ser
Ala Ala Ala Leu Phe Ser Leu Thr Val Ser Leu Asp Asp Arg Asn Ser
Ser Arg Tyr Val Ile Arg Ile Asp Gln Asp Gly Leu Thr Leu Pro Glu
Arg Thr Leu Tyr Leu Ala Gln Asp Glu Asp Ser Glu Lys Ile Leu Ala
Ala Tyr Arg Val Phe Met Glu Arg Val Leu Ser Leu Leu Gly Ala Asp
Ala Val Glu Gln Lys Ala Gln Glu Ile Leu Gln Val Glu Gln Gln Leu
Ala Asn Ile Thr Val Ser Glu Tyr Asp Asp Leu Arg Arg Asp Val Ser
Ser Met Tyr Asn Lys Val Thr Leu Gly Gln Leu Gln Lys Ile Thr Pro
His Leu Arg Trp Lys Trp Leu Leu Asp Gln Ile Phe Gln Glu Asp Phe
Ser Glu Glu Glu Glu Val Val Leu Leu Ala Thr Asp Tyr Met Gln Gln
Val Ser Gln Leu Ile Arg Ser Thr Pro His Arg Val Leu His Asn Tyr
Leu Val Trp Arg Val Val Val Val Leu Ser Glu His Leu Ser Pro Pro

FIG.2A

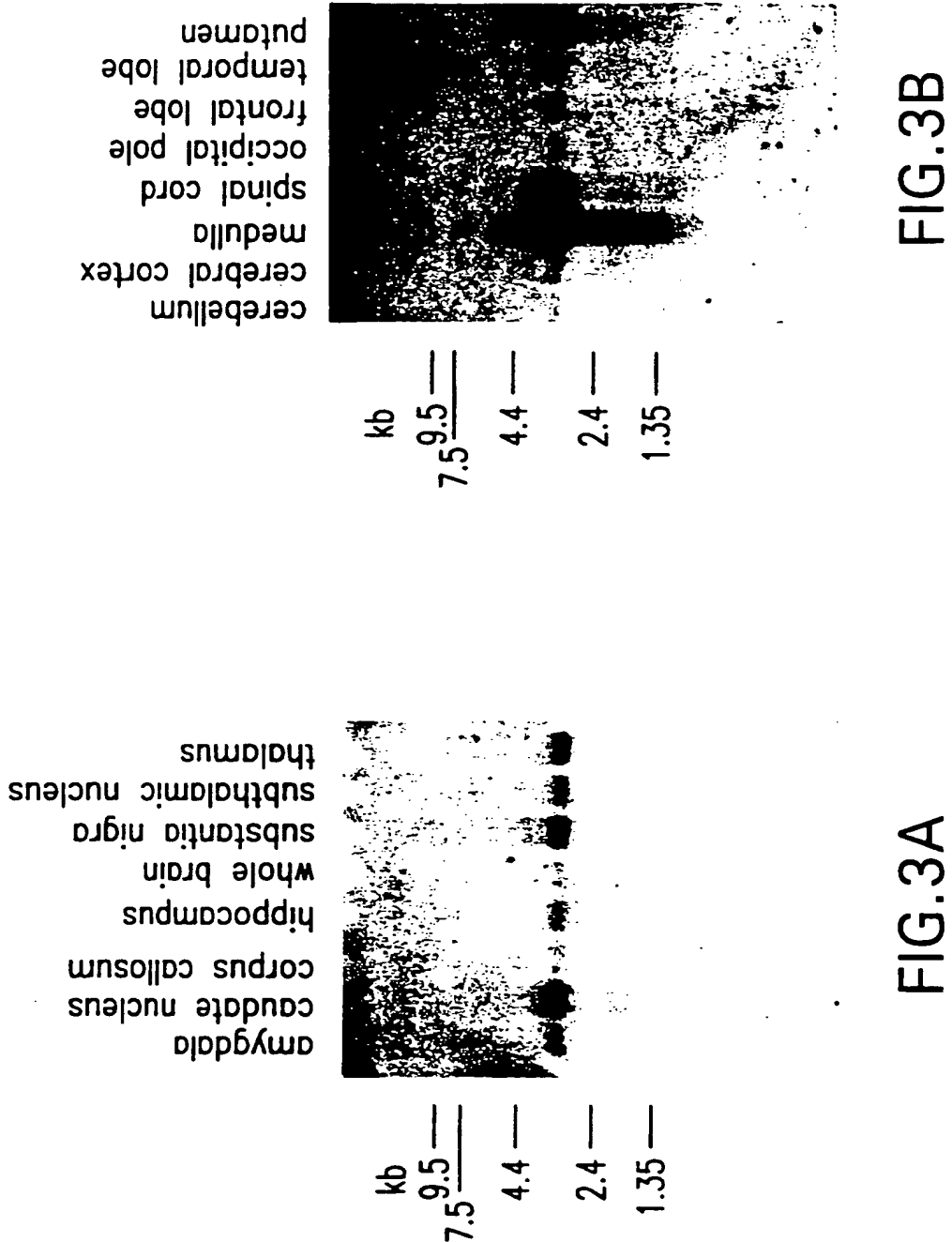
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Phe Arg Glu Ala Leu His Glu Leu Ala Gln Glu Met Glu Gly Ser Asp
Lys Pro Gln Glu Leu Ala Arg Val Cys Leu Gly Gln Ala Asn Arg His
Phe Gly Met Ala Leu Gly Ala Leu Phe Val His Glu His Phe Ser Ala
Ala Ser Lys Ala Lys Val Gln Gln Leu Val Glu Asp Ile Lys Tyr Ile
Leu Gly Gln Arg Leu Glu Glu Leu Asp Trp Met Asp Ala Glu Thr Arg
Ala Ala Ala Arg Ala Lys Leu Gln Tyr Met Met Val Met Val Gly Tyr
Pro Asp Phe Leu Leu Lys Pro Asp Ala Val Asp Lys Glu Tyr Glu Phe
Glu Val His Glu Lys Thr Tyr Phe Lys Asn Ile Leu Asn Ser Ile Arg
Phe Ser Ile Gln Leu Ser Val Lys Lys Ile Arg Gln Glu Val Asp Lys
Ser Thr Trp Leu Leu Pro Pro Gln Ala Leu Asn Ala Tyr Tyr Leu Pro
Asn Lys Asn Gln Met Val Phe Pro Ala Gly Ile Leu Gln Pro Thr Leu
Tyr Asp Pro Asp Phe Pro Gln Ser Leu Asn Tyr Gly Gly Ile Gly Thr
Ile Ile Gly His Glu Leu Thr His Gly Tyr Asp Asp Trp Gly Gly Gln
Tyr Asp Arg Ser Gly Asn Leu Leu His Trp Trp Thr Glu Ala Ser Tyr
Ser Arg Phe Leu Arg Lys Ala Glu Cys Ile Val Arg Leu Tyr Asp Asn
Phe Thr Val Tyr Asn Gln Arg Val Asn Gly Lys His Thr Leu Gly Glu
Asn Ile Ala Asp Met Gly Gly Leu Lys Leu Ala Tyr His Ala Tyr Gln
Lys Trp Val Arg Glu His Gly Pro Glu His Pro Leu Pro Arg Leu Lys
Tyr Thr His Asp Gln Leu Phe Phe Ile Ala Phe Ala Gln Asn Trp Cys
Ile Lys Arg Arg Ser Gln Ser Ile Tyr Leu Gln Val Leu Thr Asp Lys
His Ala Pro Glu His Tyr Arg Val Leu Gly Ser Val Ser Gln Phe Glu
Glu Phe Gly Arg Ala Phe His Cys Pro Lys Asp Ser Pro Met Asn Pro
Ala His Lys Cys Ser Val Trp (SEQ ID NO:2)

FIG.2B

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spleen
thymus
prostate
testis
ovary
small intestine
colon (mucosal lining)
leukocyte

kb
7.5 —
9.5 —
4.4 —
2.4 —
1.35 —

FIG.3D

heart
brain
placenta
lung
liver
skeletal muscle
kidney
pancreas

kb
7.5 —
9.5 —
4.4 —
2.4 —
1.35 —

FIG.3C

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10 20 30 40 50
GGCGGGCGGGCTGGGAGACACCGGACGCCCGCTCGGCTGCGCTGCGGGT
CCGCCGCCCGCGACCCTCTGTGGCCTGCGGGCGAGCCGACGCGACGCCGA

60 70 80 90 100
CAGGCCCCCGCTCGGGCCCCGACCGCTCGGTACCGCCGGCTCGGGCGCG
GTCCGGGGGCGAGCCCGGGCTGGGCGAGCCAGTGGCGGGCGAGCCCGCGC

110 120 130 140 150
CACCTGCCGGCTGCGGCCCCAGGGCCATGCGGAGGCCACGAGGAGGCCG
GTGGACGGCCGACGCCGGGTCCCGGTACGCCTCCGGGTGCTCCTCCGGC

160 170 180 190 200
GCGGCCACGCGCATCCCGTAGCCAGGTGGCCAGGTCTGCACCGCGGGC
CGCCGGTGCGCGTAGGGCATCGGGTCCACCGGTCCAGACGTGGCGCCGC

210 220 230 240 250
GCCTCGGCGCCATGGAGCCCCGTATTGCTGACGGCGCACTACGATGAG
CGGAGCCGCGGTACCTCGGGGGCATAAGCGACTGCCGCGTGATGCTACTC
M E P P Y S L T A H Y D E>

260 270 280 290 300
TTCCAAGAGGTCAAGTACGTGAGCCGCTGCGGCGCGGGGGGCGCGCGCG
AAGGTTCTCCAGTTCATGCACTCGGCGACGCCGCGCCCCCGCGCGCGCC
F Q E V K Y V S R C G A G G A R G>

310 320 330 340 350
GGCCTCCCTGCCCCGGGCTTCCCGTTGGGCGCTGCCCGCAGCGCCACCG
CCGGAGGGACGGGGGCCGAAGGGCAACCCGCGACGGGCGTGCGGTGGC
A S L P P G F P L G A A R S A T>

360 370 380 390 400
GGGCCCCGTCCGGGCTGCCGCGCTGGAACCGGCGCGAGGTGTGCCTGCTG
CCCGGGCCAGGCCCGACGGCGCGACCTTGGCCGCGCTCCACACGGACGAC
G A R S G L P R W N R R E V C L L>

410 420 430 440 450
TCGGGGCTGGTGTTCGCCCGCGGCTCTGCGCCATTCTGGCGGCTATGCT
AGCCCCGACCACAAGCGGCGGGCCGAGACGCGGTAAGACCGCCGATACGA
S G L V F A A G L C A I L A A M L>

FIG.4A

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460 470 480 490 500
GGCCCTCAAGTACCTGGGCCCCGGTCGCGGCCGGCGGCGGCCTGTCCCG
CCGGGAGTTCATGGACCCGGGCCAGCGCCGGCCGCCGCGGACAGGGC
A L K Y L G P V A A G G G A C P>

510 520 530 540 550
AGGGCTGCCCTGAGCGCAAGGCCTTCGCGCGCGCCGCTCGCTTCCTGGCC
TCCCGACGGGACTCGCGTTCGGGAAGCGCGCGCGGCGAGCGAAGGACCGG
E G C P E R K A F A R A A R F L A>

560 570 580 590 600
GCCAACCTGGACGCCAGCATCGACCCATGCCAGGACTTCTACTCGTTCGC
CGGTTGGACCTGCGGTCGTAGCTGGGTACGGTCCTGAAGATGAGCAAGCG
A N L D A S I D P C Q D F Y S F A>

610 620 630 640 650
CTGCGGCGGTTGGCTGCGGCGCCACGCCATCCCCGACGACAAGCTCACCT
GACGCCGCCAACCGACGCCGCGGTGCGGTAGGGGCTGCTGTTTCGAGTGGA
C G G W L R R H A I P D D K L T>

660 670 680 690 700
ATGGCACCATCGCGGCCATCGGCGAGCAAAACGAGGAGCGCCTACGGCGC
TACCGTGGTAGCGCCGGTAGCCGCTCGTTTTGCTCCTCGCGGATGCCGCG
Y G T I A A I G E Q N E E R L R R>

710 720 730 740 750
CTGCTGGCGCGGCCCGGGGTGGGCTGGCGGCGCGGCCAGCGCAAGGT
GACGACCGCGCCGGGCCCCCACC CGGACCGCGCGCGGGTCGCGTTCCA
L L A R P G G G P G G A A Q R K V>

760 770 780 790 800
GCGCGCCTTCTTCGCTCGTGCCTCGACATGCGCGAGATCGAGCGACTGG
CGCGCGGAAGAAGGCGAGCACGGAGCTGTACGCGCTCTAGCTCGCTGACC
R A F F R S C L D M R E I E R L>

810 820 830 840 850
GCCCCGACCCATGCTAGAGGTCATCGAGGACTGCGGGGGCTGGGACCTG
CGGGCGCTGGGTACGATCTCCAGTAGCTCCTGACGCCCCGACCCTGGAC
G P R P M L E V I E D C G G W D L>

FIG.4B

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860 870 880 890 900
GGCGGCGCGGAGGAGCGTCCGGGGGTGCGGGCGCGATGGGACCTCAACCG
CCGCCGCGCCTCCTCGCAGGCCCCAGCGCCGCGCTACCCTGGAGTTGGC
G G A E E R P G V A A R W D L N R>

910 920 930 940 950
GCTGCTGTACAAGGCGCAGGGCGTGTACAGCGCCGCCGCGCTCTTCTCGC
CGACGACATGTTCCGCGTCCCGCACATGTCGCGGGCGGCGCGAGAAGAGCG
L L Y K A Q G V Y S A A A L F S>

960 970 980 990 1000
TCACGGTCAGCCTGGACGACAGGAACCTCCTCGCGCTACGTCATCCGCATT
AGTGCCAGTCGGACCTGCTGTCTTGAGGAGCGCGATGCAGTAGGCGTAA
L T V S L D D R N S S R Y V I R I>

1010 1020 1030 1040 1050
GACCAGGATGGGCTCACCTGCCAGAGAGGACCCTGTACCTCGCTCAGGA
CTGGTCCTACCCGAGTGGGACGGTCTCTCCTGGGACATGGAGCGAGTCTT
D Q D G L T L P E R T L Y L A Q D>

1060 1070 1080 1090 1100
TGAGGACAGTGAGAAGATCCTGGCAGCATAACAGGGTGTTCATGGAGCGAG
ACTCCTGTCACTCTTCTAGGACCGTCGTATGTCCCACAAGTACCTCGCTC
E D S E K I L A A Y R V F M E R>

1110 1120 1130 1140 1150
TGCTCAGCCTCCTGGGTGCAGACGCTGTGGAACAGAAGGCCCAAGAGATC
ACGAGTCGGAGGACCCACGTCTGCGACACCTTGTCTTCCGGGTTCTCTAG
V L S L L G A D A V E Q K A Q E I>

1160 1170 1180 1190 1200
CTGCAAGTGGAGCAGCAGCTGGCCAACATCACTGTGTCAGAGTATGACGA
GACGTTACCTCGTCGTCGACCGGTTGTAGTGACACAGTCTCATACTGCT
L Q V E Q Q L A N I T V S E Y D D>

1210 1220 1230 1240 1250
CCTACGGCGAGATGTCAGCTCCATGTACAACAAGGTGACGCTGGGGCAGC
GGATGCCGCTCTACAGTCGAGGTACATGTTGTTCCACTGCGACCCCGTCG
L R R D V S S M Y N K V T L G Q>

FIG.4C

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1260 1270 1280 1290 1300
TGCAGAAGATCACCCCCCACTTGCGGTGGAAGTGGCTGCTAGACCAGATC
ACGTCTTCTAGTGGGGGGTGAACGCCACCTTCACCGACGATCTGGTCTAG
L Q K I T P H L R W K W L L D Q I>

1310 1320 1330 1340 1350
TTCCAGGAGGACTTCTCAGAGGAAGAGGAGGTGGTGTCTGCTGGCGACAGA
AAGGTCCTCCTGAAGAGTCTCCTTCTCCTCCACCACGACGACCGCTGTCT
F Q E D F S E E E E V V L L A T D>

1360 1370 1380 1390 1400
CTACATGCAGCAGGTGTGCGAGCTCATCCGCTCCACACCCACCGGGTCC
GATGTACGTCTCCACAGCGTCTGAGTAGGCGAGGTGTGGGGTGGCCCAGG
Y M Q Q V S Q L I R S T P H R V>

1410 1420 1430 1440 1450
TGCACAACCTACCTGGTGTGGCGCGTGGTGGTGGTCTGAGTGAACACCTG
ACGTGTTGATGGACCACACCGCGCACCAACCAGGACTCACTTGTGGAC
L H N Y L V W R V V V V L S E H L>

1460 1470 1480 1490 1500
TCCCCGCCATTCCGTGAGGCACTGCACGAGCTGGCACAGGAGATGGAGGG
AGGGGCGGTAAGGCACTCCGTGACGTGCTCGACCGTGTCTCTACCTCCC
S P P F R E A L H E L A Q E M E G>

1510 1520 1530 1540 1550
CAGCGACAAGCCACAGGAGCTGGCCCCGGGTCTGCTTGGGCCAGGCCAATC
GTCGCTGTTCCGGTGTCTCGACCGGGCCAGACGAACCCGGTCCGGTTAG
S D K P Q E L A R V C L G Q A N>

1560 1570 1580 1590 1600
GCCACTTTGGCATGGCGCTTGGCGCCCTCTTTGTACATGAGCACTTCTCA
CGGTGAAACCGTACCGCGAACCGCGGGAGAAACATGTACTCGTGAAGAGT
R H F G M A L G A L F V H E H F S>

1610 1620 1630 1640 1650
GCTGCCAGCAAAGCCAAGGTGCAGCAGCTAGTGGAAGACATCAAGTACAT
CGACGGTCGTTTCGGTTCACGTCGTCGATCACCTTCTGTAGTTCATGTA
A A S K A K V Q Q L V E D I K Y I>

FIG.4D

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1660 1670 1680 1690 1700
CCTGGGCCAGCGCCTGGAGGAGCTGGACTGGATGGACGCCGAGACCAGGG
GGACCCGGTCGCGGACCTCCTCGACCTGACCTACCTGCGGCTCTGGTCCC
L G Q R L E E L D W M D A E T R>

1710 1720 1730 1740 1750
CTGCTGCTCGGGCCAAGCTCCAGTACATGATGGTGATGGTCGGCTACCCG
GACGACGAGCCCGGTTTCGAGGTCATGTACTACCACTACCAGCCGATGGGC
A A A R A K L Q Y M M V M V G Y P>

1760 1770 1780 1790 1800
GACTTCCTGCTGAAACCCGATGCTGTGGACAAGGAGTATGAGTTTGAGGT
CTGAAGGACGACTTTGGGCTACGACACCTGTTCTCATACTCAAACCTCCA
D F L L K P D A V D K E Y E F E V>

1810 1820 1830 1840 1850
CCATGAGAAGACCTACTTCAAGAACATCTTGAACAGCATCCGCTTCAGCA
GGTACTCTTCTGGATGAAGTTCTTGTAGAACTTGTCGTAGGCCGAAGTCGT
H E K T Y F K N I L N S I R F S>

1860 1870 1880 1890 1900
TCCAGCTCTCAGTTAAGAAGATTCGGCAGGAGGTGGACAAGTCCACGTGG
AGGTTCGAGAGTCAATTCTTCTAAGCCGTCCTCCACCTGTTTCAGGTGCACC
I Q L S V K K I R Q E V D K S T W>

1910 1920 1930 1940 1950
CTGCTCCCCCACAGGCGCTCAATGCCTACTATCTACCCAACAAGAACCA
GACGAGGGGGGTGTCCGCGAGTTACGGATGATAGATGGGTTGTTCTTGGT
L L P P Q A L N A Y Y L P N K N Q>

1960 1970 1980 1990 2000
GATGGTGTTCCCCGCGGGCATCCTGCAGCCACCCTGTACGACCCTGACT
CTACCACAAGGGGCGCCCGTAGGACGTCGGGTGGGACATGCTGGGACTGA
M V F P A G I L Q P T L Y D P D>

2010 2020 2030 2040 2050
TCCCACAGTCTCTCAACTACGGGGGCATCGGCACCATCATTGGACATGAG
AGGGTGTCAGAGAGTTGATGCCCCGTCGCGTGGTAGTAACCTGTACTC
F P Q S L N Y G G I G T I I G H E>

FIG.4E

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2060 2070 2080 2090 2100
CTGACCCACGGCTACGACGACTGGGGGGGCCAGTATGACCGCTCAGGGAA
GACTGGGTGCCGATGCTGCTGACCCCCCGGTCATACTGGCGAGTCCCTT
L T H G Y D D W G G Q Y D R S G N>

2110 2120 2130 2140 2150
CCTGCTGCACTGGTGGACGGAGGCCTCCTACAGCCGCTTCCTGCGAAAGG
GGACGACGTGACCACCTGCCTCCGGAGGATGTCGGCGAAGGACGCTTTCC
L L H W W T E A S Y S R F L R K>

2160 2170 2180 2190 2200
CTGAGTGCATCGTCCGTCTCTATGACAACTTCACTGTCTACAACCAGCGG
GACTCACGTAGCAGGCAGAGATACTGTTGAAGTGACAGATGTTGGTCGCC
A E C I V R L Y D N F T V Y N Q R>

2210 2220 2230 2240 2250
GTGAACGGGAAACACACGCTTGGGGAGAACATCGCAGATATGGGCGGCCT
CACTTGCCCTTTGTGTGCGAACCCTCTTGTAGCGTCTATACCCGCCGGA
V N G K H T L G E N I A D M G G L>

2260 2270 2280 2290 2300
CAAGCTGGCCTACCACGCCTATCAGAAGTGGGTGCGGGAGCACGGCCCAG
GTTTCGACCGGATGGTGC GGATAGTCTTCACCCACGCCCTCGTGCCGGGTC
K L A Y H A Y Q K W V R E H G P>

2310 2320 2330 2340 2350
AGCACCCACTTCCCCGGCTCAAGTACACACATGACCAGCTCTTCTTCATT
TCGTGGGTGAAGGGGCCGAGTTCATGTGTGTACTGGTCGAGAAGAAGTAA
E H P L P R L K Y T H D Q L F F I>

2360 2370 2380 2390 2400
GCCTTTGCCCAGAACTGGTGCATCAAGCGGCGGTGCGAGTCCATCTACCT
CGGAAACGGGTCTTGACCACGTAGTTCGCCGCCAGCGTCAGGTAGATGGA
A F A Q N W C I K R R S Q S I Y L>

2410 2420 2430 2440 2450
GCAGGTGCTGACTGACAAGCATGCCCCTGAGCACTACAGGGTGCTGGGCA
CGTCCACGACTGACTGTTTCGTACGGGGACTCGTGATGTCCACGACCCGT
Q V L T D K H A P E H Y R V L G>

FIG.4F

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2460 2470 2480 2490 2500
GTGTGTCCCAGTTTGAGGAGTTTGGCCGGGCTTTCCACTGTCCCAAGGAC
CACACAGGGTCAAACCTCCTCAAACCGGCCCGAAAGGTGACAGGGTTCCTG
S V S Q F E E F G R A F H C P K D>

2510 2520 2530 2540 2550
TCACCCATGAACCCTGCCCACAAGTGTTCCGTGTGGTGAGCCTGGCTGCC
AGTGGGTACTTGGGACGGGTGTTTACAAGGCACACCACTCGGACCGACGG
S P M N P A H K C S V W * (SEQ ID NO:2)

2560 2570 2580 2590 2600
CGCCTGCACGCCCCCACTGCCCCGCACGAATCACCTCCTGCTGGCTACC
GCGGACGTGCGGGGGTGACGGGGGCGTGCTTAGTGAGGACGACCGATGG

2610 2620 2630 2640 2650
GGGGCAGGCATGCACCCGGTGCCAGCCCCGCTCTGGGCACCACCTGCCTT
CCCCGTCCGTACGTGGGCCACGGTCGGGGCGAGACCCGTGGTGGACGGAA

2660 2670 2680 2690 2700
CCAGCCCCTCCAGGACCCGGTCCCCCTGCTGCCCCTCACTTCAGGAGGGG
GGTCGGGGAGGTCCTGGGCCAGGGGGACGACGGGGAGTGAAGTCCTCCCC

2710 2720 2730 2740 2750
CCTGGAGCAGGGTGAGGCTGGACTTTGGGGGGCTGTGAGGGAAATATACT
GGACCTCGTCCCACTCCGACCTGAAACCCCCGACACTCCCTTTATATGA

2760 2770 2780 2790 2800
GGGGTCCCCAGATTCTGCTCTAAGGGGGCCAGACCCTCTGCCAGGCTGGA
CCCCAGGGGTCTAAGACGAGATTCCCCCGGTCTGGGAGACGGTCCGACCT

2810 2820 2830 2840 2850
TTGTACGGGCCCCACCTTCGCTGTGTTCTTGCTGCAAAGTCTGGTCAATA
AACATGCCCGGGGTGGAAGCGACACAAGAACGACGTTTCAGACCAGTTAT

2860 2870 2880 2890
AATCACTGCACTGTTAAAAAAAAAAAAAAAAAAATTCCTGCG (SEQ ID NO:1)
Ttagtgacgtgacaatttttttttttttttttttttaaggacgc (SEQ ID NO:22)

FIG.4G

SEQUENCE LISTING

<110> APPLICANT: Merck & Co., Inc.

<120> TITLE: DNA MOLECULES ENCODING HUMAN ENDOTHELIN
CONVERTING ENZYME 3

<130> DOCKET/FILE REFERENCE: 20423

<160> NUMBER OF SEQUENCES: 22

<170> SOFTWARE: FastSEQ for Windows Version 4.0

<210> SEQ ID NO:1

<211> LENGTH: 2894

<212> TYPE: DNA

<213> ORGANISM: Homo sapien

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (212)...(2536)

<400> SEQ ID NO:1

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ctcggggccc acccgctcgg tcaccgccgg ctcgggcgcg cacctgccgg ctgcggcccc      120
agggccatgc ggaggccac gaggaggccg gcggccacgc gcaccccgta gcccaggtgg      180
cccaggtctg caccgcggcg gcctcggcgc c atg gag ccc ccg tat tcg ctg      232
                               Met Glu Pro Pro Tyr Ser Leu
                               1                               5

acg gcg cac tac gat gag ttc caa gag gtc aag tac gtg agc cgc tgc      280
Thr Ala His Tyr Asp Glu Phe Gln Glu Val Lys Tyr Val Ser Arg Cys
      10                               15                               20

ggc gcg ggg ggc gcg cgc ggg gcc tcc ctg ccc ccg ggc ttc ccg ttg      328
Gly Ala Gly Gly Ala Arg Gly Ala Ser Leu Pro Gly Phe Pro Leu
      25                               30                               35

ggc gct gcc cgc agc gcc acc ggg gcc cgg tcc ggg ctg ccg cgc tgg      376
Gly Ala Ala Arg Ser Ala Thr Gly Ala Arg Ser Gly Leu Pro Arg Trp
      40                               45                               50                               55

aac cgg cgc gag gtg tgc ctg ctg tcg ggg ctg gtg ttc gcc gcc ggc      424
Asn Arg Arg Glu Val Cys Leu Leu Ser Gly Leu Val Phe Ala Ala Gly
      60                               65                               70

ctc tgc gcc att ctg gcg gct atg ctg gcc ctc aag tac ctg ggc ccg      472
Leu Cys Ala Ile Leu Ala Ala Met Leu Ala Leu Lys Tyr Leu Gly Pro
      75                               80                               85

gtc gcg gcc ggc ggc ggc gcc tgt ccc gag ggc tgc cct gag cgc aag      520
Val Ala Ala Gly Gly Gly Ala Cys Pro Glu Gly Cys Pro Glu Arg Lys
      90                               95                               100

gcc ttc gcg cgc gcc gct cgc ttc ctg gcc gcc aac ctg gac gcc agc      568
Ala Phe Ala Arg Ala Ala Arg Phe Leu Ala Ala Asn Leu Asp Ala Ser
      105                               110                               115

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atc gac cca tgc cag gac ttc tac tcg ttc gcc tgc ggc ggt tgg ctg Ile Asp Pro Cys Gln Asp Phe Tyr Ser Phe Ala Cys Gly Gly Trp Leu 120 125 130 135	616
cgg cgc cac gcc atc ccc gac gac aag ctc acc tat ggc acc atc gcg Arg Arg His Ala Ile Pro Asp Asp Lys Leu Thr Tyr Gly Thr Ile Ala 140 145 150	664
gcc atc ggc gag caa aac gag gag cgc cta cgg cgc ctg ctg gcg cgg Ala Ile Gly Glu Gln Asn Glu Glu Arg Leu Arg Arg Leu Ala Arg 155 160 165	712
ccc ggg ggt ggg cct ggc ggc gcg gcc cag cgc aag gtg cgc gcc ttc Pro Gly Gly Gly Pro Gly Gly Ala Ala Gln Arg Lys Val Arg Ala Phe 170 175 180	760
ttc cgc tcg tgc ctc gac atg cgc gag atc gag cga ctg ggc ccg cga Phe Arg Ser Cys Leu Asp Met Arg Glu Ile Glu Arg Leu Gly Pro Arg 185 190 195	808
ccc atg cta gag gtc atc gag gac tgc ggg ggc tgg gac ctg ggc ggc Pro Met Leu Glu Val Ile Glu Asp Cys Gly Gly Trp Asp Leu Gly Gly 200 205 210 215	856
gcg gag gag cgt ccg ggg gtc gcg gcg cga tgg gac ctc aac cgg ctg Ala Glu Glu Arg Pro Gly Val Ala Ala Arg Trp Asp Leu Asn Arg Leu 220 225 230	904
ctg tac aag gcg cag ggc gtg tac agc gcc gcc gcg ctc ttc tcg ctc Leu Tyr Lys Ala Gln Gly Val Tyr Ser Ala Ala Ala Leu Phe Ser Leu 235 240 245	952
acg gtc agc ctg gac gac agg aac tcc tcg cgc tac gtc atc cgc att Thr Val Ser Leu Asp Asp Arg Asn Ser Ser Arg Tyr Val Ile Arg Ile 250 255 260	1000
gac cag gat ggg ctc acc ctg cca gag agg acc ctg tac ctc gct cag Asp Gln Asp Gly Leu Thr Leu Pro Glu Arg Thr Leu Tyr Leu Ala Gln 265 270 275	1048
gat gag gac agt gag aag atc ctg gca gca tac agg gtg ttc atg gag Asp Glu Asp Ser Glu Lys Ile Leu Ala Ala Tyr Arg Val Phe Met Glu 280 285 290 295	1096
cga gtg ctc agc ctc ctg ggt gca gac gct gtg gaa cag aag gcc caa Arg Val Leu Ser Leu Leu Gly Ala Asp Ala Val Glu Gln Lys Ala Gln 300 305 310	1144
gag atc ctg caa gtg gag cag cag ctg gcc aac atc act gtg tca gag Glu Ile Leu Gln Val Glu Gln Gln Leu Ala Asn Ile Thr Val Ser Glu 315 320 325	1192
tat gac gac cta cgg cga gat gtc agc tcc atg tac aac aag gtg acg Tyr Asp Asp Leu Arg Arg Asp Val Ser Ser Met Tyr Asn Lys Val Thr 330 335 340	1240
ctg ggg cag ctg cag aag atc acc ccc cac ttg cgg tgg aag tgg ctg Leu Gly Gln Leu Gln Lys Ile Thr Pro His Leu Arg Trp Lys Trp Leu 345 350 355	1288

cta gac cag atc ttc cag gag gac ttc tca gag gaa gag gag gtg gtg	1336
Leu Asp Gln Ile Phe Gln Glu Asp Phe Ser Glu Glu Glu Val Val	
360 365 370 375	
ctg ctg gcg aca gac tac atg cag cag gtg tcg cag ctc atc cgc tcc	1384
Leu Leu Ala Thr Asp Tyr Met Gln Gln Val Ser Gln Leu Ile Arg Ser	
380 385 390	
aca ccc cac cgg gtc ctg cac aac tac ctg gtg tgg cgc gtg gtg gtg	1432
Thr Pro His Arg Val Leu His Asn Tyr Leu Val Trp Arg Val Val Val	
395 400 405	
gtc ctg agt gaa cac ctg tcc ccg cca ttc cgt gag gca ctg cac gag	1480
Val Leu Ser Glu His Leu Ser Pro Pro Phe Arg Glu Ala Leu His Glu	
410 415 420	
ctg gca cag gag atg gag ggc agc gac aag cca cag gag ctg gcc cgg	1528
Leu Ala Gln Glu Met Glu Gly Ser Asp Lys Pro Gln Glu Leu Ala Arg	
425 430 435	
gtc tgc ttg ggc cag gcc aat cgc cac ttt ggc atg gcg ctt ggc gcc	1576
Val Cys Leu Gly Gln Ala Asn Arg His Phe Gly Met Ala Leu Gly Ala	
440 445 450 455	
ctc ttt gta cat gag cac ttc tca gct gcc agc aaa gcc aag gtg cag	1624
Leu Phe Val His Glu His Phe Ser Ala Ala Ser Lys Ala Lys Val Gln	
460 465 470	
cag cta gtg gaa gac atc aag tac atc ctg ggc cag cgc ctg gag gag	1672
Gln Leu Val Glu Asp Ile Lys Tyr Ile Leu Gly Gln Arg Leu Glu Glu	
475 480 485	
ctg gac tgg atg gac gcc gag acc agg gct gct gct cgg gcc aag ctc	1720
Leu Asp Trp Met Asp Ala Glu Thr Arg Ala Ala Ala Arg Ala Lys Leu	
490 495 500	
cag tac atg atg gtg atg gtc ggc tac ccg gac ttc ctg ctg aaa ccc	1768
Gln Tyr Met Met Val Met Val Gly Tyr Pro Asp Phe Leu Leu Lys Pro	
505 510 515	
gat gct gtg gac aag gag tat gag ttt gag gtc cat gag aag acc tac	1816
Asp Ala Val Asp Lys Glu Tyr Glu Phe Glu Val His Glu Lys Thr Tyr	
520 525 530 535	
ttc aag aac atc ttg aac agc atc cgc ttc agc atc cag ctc tca gtt	1864
Phe Lys Asn Ile Leu Asn Ser Ile Arg Phe Ser Ile Gln Leu Ser Val	
540 545 550	
aag aag att cgg cag gag gtg gac aag tcc acg tgg ctg ctc ccc cca	1912
Lys Lys Ile Arg Gln Glu Val Asp Lys Ser Thr Trp Leu Leu Pro Pro	
555 560 565	
cag gcg ctc aat gcc tac tat cta ccc aac aag aac cag atg gtg ttc	1960
Gln Ala Leu Asn Ala Tyr Tyr Leu Pro Asn Lys Asn Gln Met Val Phe	
570 575 580	
ccc gcg ggc atc ctg cag ccc acc ctg tac gac cct gac ttc cca cag	2008
Pro Ala Gly Ile Leu Gln Pro Thr Leu Tyr Asp Pro Asp Phe Pro Gln	
585 590 595	

tct ctc aac tac ggg ggc atc ggc acc atc att gga cat gag ctg acc	2056
Ser Leu Asn Tyr Gly Gly Ile Gly Thr Ile Ile Gly His Glu Leu Thr	
600 605 610 615	
cac ggc tac gac gac tgg ggg ggc cag tat gac cgc tca ggg aac ctg	2104
His Gly Tyr Asp Asp Trp Gly Gly Gln Tyr Asp Arg Ser Gly Asn Leu	
620 625 630	
ctg cac tgg tgg acg gag gcc tcc tac agc cgc ttc ctg cga aag gct	2152
Leu His Trp Trp Thr Glu Ala Ser Tyr Ser Arg Phe Leu Arg Lys Ala	
635 640 645	
gag tgc atc gtc cgt ctc tat gac aac ttc act gtc tac aac cag cgg	2200
Glu Cys Ile Val Arg Leu Tyr Asp Asn Phe Thr Val Tyr Asn Gln Arg	
650 655 660	
gtg aac ggg aaa cac acg ctt ggg gag aac atc gca gat atg ggc ggc	2248
Val Asn Gly Lys His Thr Leu Gly Glu Asn Ile Ala Asp Met Gly Gly	
665 670 675	
ctc aag ctg gcc tac cac gcc tat cag aag tgg gtg cgg gag cac ggc	2296
Leu Lys Leu Ala Tyr His Ala Tyr Gln Lys Trp Val Arg Glu His Gly	
680 685 690 695	
cca gag cac cca ctt ccc cgg ctc aag tac aca cat gac cag ctc ttc	2344
Pro Glu His Pro Leu Pro Arg Leu Lys Tyr Thr His Asp Gln Leu Phe	
700 705 710	
ttc att gcc ttt gcc cag aac tgg tgc atc aag cgg cgg tcg cag tcc	2392
Phe Ile Ala Phe Ala Gln Asn Trp Cys Ile Lys Arg Arg Ser Gln Ser	
715 720 725	
atc tac ctg cag gtg ctg act gac aag cat gcc cct gag cac tac agg	2440
Ile Tyr Leu Gln Val Leu Thr Asp Lys His Ala Pro Glu His Tyr Arg	
730 735 740	
gtg ctg ggc agt gtg tcc cag ttt gag gag ttt ggc cgg gct ttc cac	2488
Val Leu Gly Ser Val Ser Gln Phe Glu Glu Phe Gly Arg Ala Phe His	
745 750 755	
tgt ccc aag gac tca ccc atg aac cct gcc cac aag tgt tcc gtg tgg	2536
Cys Pro Lys Asp Ser Pro Met Asn Pro Ala His Lys Cys Ser Val Trp	
760 765 770 775	
tgagcctggc tgcccgcctg cagcccccca ctgccccgc acgaatcacc tctgtctggc	2596
taccgggggca ggcatgcacc cggtgccagc ccgctctgg gcaccacctg ccttccagcc	2656
cctccaggac ccggtccccc tctgcccct cacttcagga ggggcctgga gcagggtgag	2716
gctggacttt ggggggctgt gagggaaata tactggggtc cccagattct gctctaaggg	2776
ggccagaccc tctgccaggc tggattgtac gggccccacc ttcgctgtgt tcttctgtgca	2836
aagtctggtc aataaatcac tgcactgtta aaaaaaaaaa aaaaaaaaaa ttcctgcg	2894

<210> SEQ ID NO:2

<211> LENGTH: 775

<212> TYPE: PRT

<213> ORGANISM:Homo sapien

<400> SEQ ID NO:2

Met Glu Pro Pro Tyr Ser Leu Thr Ala His Tyr Asp Glu Phe Gln Glu	
1 5 10 15	
Val Lys Tyr Val Ser Arg Cys Gly Ala Gly Gly Ala Arg Gly Ala Ser	
20 25 30	

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Leu Pro Pro Gly Phe Pro Leu Gly Ala Ala Arg Ser Ala Thr Gly Ala
    35          40          45
Arg Ser Gly Leu Pro Arg Trp Asn Arg Arg Glu Val Cys Leu Leu Ser
    50          55          60
Gly Leu Val Phe Ala Ala Gly Leu Cys Ala Ile Leu Ala Ala Met Leu
65          70          75          80
Ala Leu Lys Tyr Leu Gly Pro Val Ala Ala Gly Gly Gly Ala Cys Pro
    85          90          95
Glu Gly Cys Pro Glu Arg Lys Ala Phe Ala Arg Ala Ala Arg Phe Leu
    100          105          110
Ala Ala Asn Leu Asp Ala Ser Ile Asp Pro Cys Gln Asp Phe Tyr Ser
    115          120          125
Phe Ala Cys Gly Gly Trp Leu Arg Arg His Ala Ile Pro Asp Asp Lys
    130          135          140
Leu Thr Tyr Gly Thr Ile Ala Ala Ile Gly Glu Gln Asn Glu Glu Arg
145          150          155          160
Leu Arg Arg Leu Leu Ala Arg Pro Gly Gly Pro Gly Gly Ala Ala
    165          170          175
Gln Arg Lys Val Arg Ala Phe Phe Arg Ser Cys Leu Asp Met Arg Glu
    180          185          190
Ile Glu Arg Leu Gly Pro Arg Pro Met Leu Glu Val Ile Glu Asp Cys
    195          200          205
Gly Gly Trp Asp Leu Gly Gly Ala Glu Glu Arg Pro Gly Val Ala Ala
    210          215          220
Arg Trp Asp Leu Asn Arg Leu Leu Tyr Lys Ala Gln Gly Val Tyr Ser
225          230          235          240
Ala Ala Ala Leu Phe Ser Leu Thr Val Ser Leu Asp Asp Arg Asn Ser
    245          250          255-
Ser Arg Tyr Val Ile Arg Ile Asp Gln Asp Gly Leu Thr Leu Pro Glu
    260          265          270
Arg Thr Leu Tyr Leu Ala Gln Asp Glu Asp Ser Glu Lys Ile Leu Ala
    275          280          285
Ala Tyr Arg Val Phe Met Glu Arg Val Leu Ser Leu Leu Gly Ala Asp
    290          295          300
Ala Val Glu Gln Lys Ala Gln Glu Ile Leu Gln Val Glu Gln Gln Leu
305          310          315          320
Ala Asn Ile Thr Val Ser Glu Tyr Asp Asp Leu Arg Arg Asp Val Ser
    325          330          335
Ser Met Tyr Asn Lys Val Thr Leu Gly Gln Leu Gln Lys Ile Thr Pro
    340          345          350
His Leu Arg Trp Lys Trp Leu Leu Asp Gln Ile Phe Gln Glu Asp Phe
    355          360          365
Ser Glu Glu Glu Glu Val Val Leu Leu Ala Thr Asp Tyr Met Gln Gln
    370          375          380
Val Ser Gln Leu Ile Arg Ser Thr Pro His Arg Val Leu His Asn Tyr
385          390          395          400
Leu Val Trp Arg Val Val Val Val Leu Ser Glu His Leu Ser Pro Pro
    405          410          415
Phe Arg Glu Ala Leu His Glu Leu Ala Gln Glu Met Glu Gly Ser Asp
    420          425          430
Lys Pro Gln Glu Leu Ala Arg Val Cys Leu Gly Gln Ala Asn Arg His
    435          440          445
Phe Gly Met Ala Leu Gly Ala Leu Phe Val His Glu His Phe Ser Ala
    450          455          460
Ala Ser Lys Ala Lys Val Gln Gln Leu Val Glu Asp Ile Lys Tyr Ile
465          470          475          480
Leu Gly Gln Arg Leu Glu Glu Leu Asp Trp Met Asp Ala Glu Thr Arg
    485          490          495
Ala Ala Ala Arg Ala Lys Leu Gln Tyr Met Met Val Met Val Gly Tyr
    500          505          510

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Pro Asp Phe Leu Leu Lys Pro Asp Ala Val Asp Lys Glu Tyr Glu Phe
      515                      520                      525
Glu Val His Glu Lys Thr Tyr Phe Lys Asn Ile Leu Asn Ser Ile Arg
      530                      535                      540
Phe Ser Ile Gln Leu Ser Val Lys Lys Ile Arg Gln Glu Val Asp Lys
545                      550                      555                      560
Ser Thr Trp Leu Leu Pro Pro Gln Ala Leu Asn Ala Tyr Tyr Leu Pro
      565                      570                      575
Asn Lys Asn Gln Met Val Phe Pro Ala Gly Ile Leu Gln Pro Thr Leu
      580                      585                      590
Tyr Asp Pro Asp Phe Pro Gln Ser Leu Asn Tyr Gly Gly Ile Gly Thr
      595                      600                      605
Ile Ile Gly His Glu Leu Thr His Gly Tyr Asp Asp Trp Gly Gly Gln
      610                      615                      620
Tyr Asp Arg Ser Gly Asn Leu Leu His Trp Trp Thr Glu Ala Ser Tyr
625                      630                      635                      640
Ser Arg Phe Leu Arg Lys Ala Glu Cys Ile Val Arg Leu Tyr Asp Asn
      645                      650                      655
Phe Thr Val Tyr Asn Gln Arg Val Asn Gly Lys His Thr Leu Gly Glu
      660                      665                      670
Asn Ile Ala Asp Met Gly Gly Leu Lys Leu Ala Tyr His Ala Tyr Gln
      675                      680                      685
Lys Trp Val Arg Glu His Gly Pro Glu His Pro Leu Pro Arg Leu Lys
      690                      695                      700
Tyr Thr His Asp Gln Leu Phe Phe Ile Ala Phe Ala Gln Asn Trp Cys
705                      710                      715                      720
Ile Lys Arg Arg Ser Gln Ser Ile Tyr Leu Gln Val Leu Thr Asp Lys
      725                      730                      735
His Ala Pro Glu His Tyr Arg Val Leu Gly Ser Val Ser Gln Phe Glu
      740                      745                      750
Glu Phe Gly Arg Ala Phe His Cys Pro Lys Asp Ser Pro Met Asn Pro
      755                      760                      765
Ala His Lys Cys Ser Val Trp
      770                      775

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<210> SEQ ID NO:3

<211> LENGTH: 495

<212> TYPE: DNA

<213> ORGANISM:Homo sapien

<220> FEATURE:

<223> OTHER INFORMATION: n=T,C,A or G (any)

<400> SEQ ID NO:3

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gcccccttag agcagaatct ggggacccca gtatatctcc ctcacagccc cccaaagtcc      120
agcctcacc cgtctccaggc ccctcctgaa gtgaggggca gcagggggac cgggtcctgg      180
aggggctgga aggcaggtgg tgcccagagc ggggctggca ccgggtgcat gcctgccccg      240
gtagccagca ggaggtgatt cgtgcggggg cagtgggggc gtgcaggcgg gcagcaaggc      300
tcaccacacg gaacacttgt gggcagggtt catgggtgag tccttgggac agtggaaagc      360
ccggccaaac tcctcaaact gngacacact gccagcacc ctgtagtgt caggggcatg      420
cttgctagtc agcaactgca ggtagatgga ctgcgaccgc gcttgatgca cagttttggg      480
aaaaggcatt aaaag                                     495

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<210> SEQ ID NO:4

<211> LENGTH: 606

<212> TYPE: DNA

<213> ORGANISM:Homo sapien

<220> FEATURE:

<223> OTHER INFORMATION: n=T,C,A or G (any)

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 ggtccatgag aagacctact tcaagaacat cttgaacagc atccgcttca gcatccagct 120
 ctcagtttaag aagattcggc aggagggtga caagtccacg tggctgctcc cccacaggc 180
 gctcaatgcc tactatctac ccaacaagaa ccagatggtg ttccccgcgg gcatcctgca 240
 gccaccctg tacgacctg acttcccaca gtctctcaac tacgggggca tcggcaccat 300
 cattggacat gagctgacct acggctacga cggactgggg gggccagtat gaccgctcag 360
 ggaacctgct tgcactggtg ggacggaggc ttccttacag ccgntttcct gcgaaaggct 420
 gagtgcacg ttccctnttt tatggacaac tttcaatgtn ttacaaccag gcggtgaacg 480
 ggaaacacan gtttgggaga acatcgagc atggggcggn ctttaagttg cttaccacgc 540
 tattagagtt ggttncggga nggccccagg agcaccattt cccggttaaa tacanactga 600
 accagt 606

<210> SEQ ID NO:5
 <211> LENGTH: 352
 <212> TYPE: DNA
 <213> ORGANISM:Homo sapien
 <220> FEATURE:
 <223> OTHER INFORMATION: n=T,C,A or G (any)

<400> SEQ ID NO:5
 tttttttttt taacagtgcg gtgatttatt gaccagactt tgcagcaaga acacagcgaa 60
 ggtggggccc gtacaatcca gcctggcaga gggcttgccc cccttagagc agaatctggg 120
 gaccccagta tatttccctc acagccccc aaagtccagc ctcaccctgc tccaggcccc 180
 tcctgaagtg aggggcagca gggggaccgg agtcctggag gggctggaag gcagggtggtg 240
 cccagagcgg ggctggcacc ggggtgcatg ctgccccggt agccagcagg aggtgnattcg 300
 tncggggggca gtnggggcnt gcaggcgggc ancaggnttc accacacgga ac 352

<210> SEQ ID NO:6
 <211> LENGTH: 22
 <212> TYPE: DNA
 <213> ORGANISM:Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: oligonucleotide

<400> SEQ ID NO:6
 gaagtcaggg tcgtacaggg tg 22

<210> SEQ ID NO:7
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM:Artificial Sequence

<220> FEATURE:
 <223> OTHER INFORMATION: oligonucleotide

<400> SEQ ID NO:7
 cttgttgggt agatagtagg c 21

<210> SEQ ID NO:8
 <211> LENGTH: 25
 <212> TYPE: DNA
 <213> ORGANISM:Artificial Sequence

<220> FEATURE:
 <223> OTHER INFORMATION: oligonucleotide

<400> SEQ ID NO:8
ctggatgctg aagcggatgc tggtc 25

<210> SEQ ID NO:9
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM:Artificial Sequence

<220> FEATURE:
<223> OTHER INFORMATION: oligonucleotide

<400> SEQ ID NO:9
cctcaaactc atactccttg tccac 25

<210> SEQ ID NO:10
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM:Artificial Sequence

<220> FEATURE:
<223> OTHER INFORMATION: oligonucleotide

<400> SEQ ID NO:10
ccttggtgta catggagctg acatc 25

<210> SEQ ID NO:11
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM:Artificial Sequence

<220> FEATURE:
<223> OTHER INFORMATION: oligonucleotide

<400> SEQ ID NO:11
ccttctgttc cacagcgtct gcac 24

<210> SEQ ID NO:12
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM:Artificial Sequence

<220> FEATURE:
<223> OTHER INFORMATION: oligonucleotide

<400> SEQ ID NO:12
ggtgagccca tcttggtaa tgcg 24

<210> SEQ ID NO:13
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM:Artificial Sequence

<220> FEATURE:
<223> OTHER INFORMATION: oligonucleotide

<400> SEQ ID NO:13
gctcggtgc gctgcggctc ag 22

<210> SEQ ID NO:14
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM:Artificial Sequence

<220> FEATURE:
<223> OTHER INFORMATION: oligonucleotide

<400> SEQ ID NO:14
ggtcctggag gggctggaag g

21

<210> SEQ ID NO:15
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM:Artificial Sequence

<220> FEATURE:
<223> OTHER INFORMATION: oligonucleotide

<400> SEQ ID NO:15
catcccgtag cccagggtggc

20

<210> SEQ ID NO:16
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM:Artificial Sequence

<220> FEATURE:
<223> OTHER INFORMATION: oligonucleotide

<400> SEQ ID NO:16
gccagcagga ggtgattcgt gcg

23

<210> SEQ ID NO:17
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM:Artificial Sequence

<220> FEATURE:
<223> OTHER INFORMATION: oligonucleotide

<400> SEQ ID NO:17
gtccccctgc tgccccctcac ttcag

25

<210> SEQ ID NO:18
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM:Artificial Sequence

<220> FEATURE:
<223> OTHER INFORMATION: oligonucleotide

<400> SEQ ID NO:18
ccagactttg cagcaagaac acagc

25

<210> SEQ ID NO:19
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM:Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: oligonucleotide

<400> SEQ ID NO:19
cttcctgctg aaacccgatg c

21

<210> SEQ ID NO:20
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM:Artificial Sequence

<220> FEATURE:
<223> OTHER INFORMATION: oligonucleotide

<400> SEQ ID NO:20
ccagactttg cagcaagaac acagc

25

<210> SEQ ID NO:21
<211> LENGTH: 1092
<212> TYPE: DNA
<213> ORGANISM:Homo sapien

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